4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATCAGAA
     TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
                                    ^

4893 BGL2,

     ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
     GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
                                    ^

4954 NCOI,

     SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG
     TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
                                    ^   ^

5015 SPHI, 5035 KPNI,

     ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
     GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
                                ^   ^

5064 APAI, 5091 BALI,

     GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
     CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
                       ^

5113 NDEI,

     LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
5162 CTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
     GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATG
                      ^^   ^   ^

5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

     SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
     TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
                         ^

5240 DRA3,

     LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT
     GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
                       ^

5295 PSTI,

     ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCCGCAGGACGTCAAGTTC
     GGATTTGGAGTTTCTTTCTGGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG
                                        ^^   ^   ^

5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,

     ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
5402 CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
     GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC
                                                      ^

FIG. 22-Page 9

4229 DRD1, 4236 ALWN1,

```
        GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
4262    GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
        CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG
                                              ^          ^
```

4301 BGLI, 4308 BALI,

```
        LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322    CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
        GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG
                          ^
```

4345 APAI,

```
        TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
4382    TATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
        ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG
```

```
        TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
4442    TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
        ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC
                  ^
```

4452 SMAI XMAI,

```
        CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502    TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
        ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
                  ^    ^
```

4508 DRD1, 4511 TTH3I,

```
        LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
4562    CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCACAA
        GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGGACCCCTGGGGGGTGTT
```

```
        ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
4622    CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
        GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG
                  ^
```

4637 SACI,

```
        GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
4682    GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT
        CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA
                                                          ^
```

4731 NRUI,

```
        AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
4742    GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
        CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
```

```
        AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
4802    GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC
        CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
                  ^^
```

4806 PFLM1, 4807 DRA3,

```
        ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu
```

FIG. 22-Page 8

3589 DRA3, 3600 SAC2,

```
      AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
3602  GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT
      CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
```

3611 ALWN1, 3655 PFLM1,

```
      LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
3662  TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC
      AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
```

3681 DRA3,

```
      ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
3722  AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG
      TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
```

```
      SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
3782  TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC
      AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
```

3816 HIND3,

```
      SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
3842  TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
      AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
```

3875 AAT2, 3890 BGLI,

```
      ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
3902  GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
      CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
```

```
      ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
3962  ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG
      TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
```

```
      ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
4022  CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG
      GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
```

```
      TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
4082  TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
      ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
```

```
      SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
4142  TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
      AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
```

4160 ECORI,

```
      GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
4202  GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
      CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC
```

FIG. 22-Page 7

```
          ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
    2942  ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
          TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
                                         ^   ^
          2966 ESP1, 2969 SACI,


          GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
    3002  GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC
          CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG


          PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
    3062  TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG
          AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
                                              ^
          3096 BGL2,


          ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
    3122  CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC
          GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG
                                   ^                  ^
          3143 ALWN1, 3164 EAG1 XMA3,


          ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
    3182  CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG
          GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC
                                                 ^               ^
          3217 HGIE2, 3229 NCOI,


          LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
    3242  CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC
          GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG


          ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
    3302  ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
          TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
                                              ^               ^
          3332 SACI, 3346 HIND3,


          SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
    3362  TCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGC
          AGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCG


          CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
    3422  TGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCCTGGAGGGGGAGCCT
          ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
                        ^
          3437 EAM11051,


          GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
    3482  GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
          CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
               ^^ ^
          3484 BAMHI, 3485 BSAB1, 3487 BSPE1,


          AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
    3542  GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC
          CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG
```

FIG. 22-Page 6

3589 DRA3, 3600 SAC2,

```
      AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
3602  GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT
      CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
```

3611 ALWN1, 3655 PFLM1,

```
      LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
3662  TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC
      AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
```

3681 DRA3,

```
      ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
3722  AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG
      TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
```

```
      SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
3782  TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC
      AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
```

3816 HIND3,

```
      SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
3842  TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
      AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
```

3875 AAT2, 3890 BGLI,

```
      ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
3902  GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
      CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
```

```
      ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
3962  ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG
      TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
```

```
      ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
4022  CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG
      GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
```

```
      TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
4082  TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
      ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
```

```
      SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
4142  TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
      AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
```

4160 ECORI,

```
      GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
4202  GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
      CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC
```

FIG. 21-Page 7

```
      LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
2342  AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC
      TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG


      ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
2402  ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
      TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
                                  ^                ^        ^^
      2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,


      TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
2462  TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG
      ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
                                  ^                    ^
      2480 ASE1, 2497 APAI,


      ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
2522  CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
      GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
                                              ^
      2553 PSTI,


      ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
2582  GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
      CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
                          ^
      2594 DRA3,


      ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
2642  GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC
      CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG


      ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
2702  CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
      GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
                                                              ^
      2757 HGIE2,


      ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762  GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
      CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
                                                          ^
      2809 AAT2,


      ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
2822  ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
      TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
                                                  ^
      2850 EAG1 XMA3,


      ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
2882  CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
      GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
                  ^                ^
      2889 BALI, 2903 NHEI,
```

FIG. 22–Page 5

ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
1742 GTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCT
CACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGA
                                                          ^

1794 ESP1,

GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
1802 GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT
CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA
^

1802 KAS1 NARI,

GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
1862 GGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC
CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
                        ^   ^

1878 SACI, 1899 BSPH1,

ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
                    ^

1928 TTH3I,

ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
1982 GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG
CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCGTCACGTCACC
                          ^   ^

2004 NAEI, 2017 SMAI XMAI,

MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
2042 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
                    ^   ^

2067 SMAI XMAI, 2093 DRA3,

ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
2102 CCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
                ^   ^

2115 PVU2, 2159 ALWN1,

LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
2162 CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC
GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
               ^   ^

2164 MST2, 2220 ECON1,

TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
2222 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT

LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
2282 AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT
TTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCATA
                ^   ^

2285 ESP1, 2300 PVU2, 2310 BAMHI,

FIG. 22-Page 4

```
          ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
     2942 ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
          TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
                               ^   ^
          2966 ESP1, 2969 SACI,

          GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
     3002 GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC
          CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG

          PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
     3062 TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG
          AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
                                            ^
          3096 BGL2,

          ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
     3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC
          GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG
                               ^                      ^
          3143 ALWN1, 3164 EAG1 XMA3,

          ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
     3182 CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG
          GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC
                                            ^                ^
          3217 HGIE2, 3229 NCOI,

          LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
     3242 CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC
          GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG

          ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
     3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
          TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
                                            ^                ^
          3332 SACI, 3346 HIND3,

          SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
     3362 TCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGC
          AGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCG

          CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
     3422 TGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCT
          ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
                         ^
          3437 EAM11051,

          GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
     3482 GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
          CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
                ^^ ^
          3484 BAMHI, 3485 BSAB1, 3487 BSPE1,

          AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
     3542 GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC
          CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG
```

FIG. 21-Page 6

```
          LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
2342   AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC
       TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG


          ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
2402   ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
       TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
                              ^                   ^        ^^
       2425 BSAB1,  2441 AVR2,  2448 SSE83871, 2449 PSTI,


          TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
2462   TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG
       ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
                              ^                   ^
       2480 ASE1,  2497 APAI,


          ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
2522   CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
       GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
                                            ^
       2553 PSTI,


          ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
2582   GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
       CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
                              ^
       2594 DRA3,


          ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
2642   GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC
       CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG


          ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
2702   CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
       GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
                                                           ^
       2757 HGIE2,


          ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762   GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
       CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
                                                           ^
       2809 AAT2,


          ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
2822   ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
       TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
                              ^
       2850 EAG1 XMA3,


          ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
2882   CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
       GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
                ^             ^
       2889 BALI,  2903 NHEI,
```

FIG. 21-Page 5

```
      ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
1742  GTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCT
      CACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGA
                                                          ^
1794 ESP1,


      GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
1802  GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT
      CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA
      ^
1802 KAS1 NARI,


      GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
1862  GGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC
      CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
                       ^                         ^
1878 SACI, 1899 BSPH1,


      ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
1922  ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
      TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
                 ^
1928 TTH3I,


      ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
1982  GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG
      CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC
                            ^              ^
2004 NAEI, 2017 SMAI XMAI,


      MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
2042  ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
      TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
                      ^                          ^
2067 SMAI XMAI, 2093 DRA3,


      ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
2102  CCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
      GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
                   ^                                          ^
2115 PVU2, 2159 ALWN1,


      LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
2162  CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC
      GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
           ^                                             ^
2164 MST2, 2220 ECON1,


      TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
2222  TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
      ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT


      LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
2282  AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT
      TTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCATA
           ^               ^              ^
2285 ESP1, 2300 PVU2, 2310 BAMHI,
```

FIG. 21-Page 4

```
                TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTC


        ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
  1142  CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
        GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
                  ^
        1150 NCOI,


        ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
  1202  ACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTC
        TGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG
                                    ^     ^  ^        ^     ^
        1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,


        ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
  1262  GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG
        CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC


        SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
  1322  TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
        AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
                                                             ^
        1369 NAEI,


        ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
  1382  CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
        GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTGAAT
                 ^
        1385 DRD1,


        ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
  1442  CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
        GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG


        LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
  1502  CTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
        GACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT
        ^       ^
        1502 PSTI, 1507 TTH3I,


        LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
  1562  AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
        TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC
                 ^                          ^
        1565 XHOI, 1586 NDEI,


        AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
  1622  GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
        CGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
                                   ^                                ^
        1643 BSTE2, 1677 ALWN1 PVU2,


        AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
  1682  GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
        CGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC
```

<div align="center">

FIG. 22–Page 3

</div>

```
        SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
482     TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
        AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC

        AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
542     GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG
        CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC
                 ^              ^
        550 SAC2, 560 DRD1,

        AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
602     GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
        CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
                           ^
        615 BSPH1,

        ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
662     ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATC
        TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG

        ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
722     ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGGCAGGACTGGCAGGGGGAAG
        TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC

        ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
782     CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCC
        GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
                                    ^                        ^
        816 BGLI, 833 DRD1,

        ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
842     GTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACT
        CAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGA
                                             ^
        881 SACI,

        ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902     ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
        TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA
                                          ^
        931 SMAI XMAI,

        GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
962     GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG
        CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
                                          ^
        985 STUI,

        ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022    ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
        TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
                                                           ^
        1069 DRA3,

        ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
1082    AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG
```

FIG. 22-Page 2

TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTC

```
      ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
1142  CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
      GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
         ^
1150  NCOI,
```

```
      ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
1202  ACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTC
      TGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG
                                  ^   ^   ^        ^     ^
1230  BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
```

```
      ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
1262  GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG
      CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC
```

```
      SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
1322  TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
      AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
                                                        ^
1369  NAEI,
```

```
      ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
1382  CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
      GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTGAAT
         ^
1385  DRD1,
```

```
      ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
1442  CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
      GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
```

```
      LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
1502  CTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
      GACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT
      ^     ^
1502  PSTI, 1507 TTH3I,
```

```
      LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
1562  AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
      TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC
      ^                          ^
1565  XHOI, 1586 NDEI,
```

```
      AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
1622  GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
      CGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
                   ^                                            ^
1643  BSTE2, 1677 ALWN1 PVU2,
```

```
      AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
1682  GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
      CGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC
```

FIG. 21-Page 3

```
          TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC


          SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
3782      TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC
          AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
                                               ^

3816 HIND3,


          SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
3842      TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
          AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
                                          ^                   ^

3875 AAT2, 3890 BGLI,


          ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
3902      GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
          CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG


          ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
3962      ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG
          TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC


          ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
4022      CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG
          GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC


          TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
4082      TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
          ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG


          SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
4142      TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
          AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
                                    ^

4160 ECORI,


          GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
4202      GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
          CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC
                                    ^           ^

4229 DRD1, 4236 ALWN1,


          GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
4262      GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
          CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG
                                              ^           ^

4301 BGLI, 4308 BALI,


          LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322      CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
          GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG
                                               ^

4345 APAI,


          TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
4382      TATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
          ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG
```

FIG. 18–Page 7

```
       SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
482    TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
       AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC

       AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
542    GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG
       CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC
                       ^                 ^
       550 SAC2,  560 DRD1,

       AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
602    GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
       CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
                      ^
       615 BSPH1,

       ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
662    ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATC
       TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG

       ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
722    ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
       TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC

       ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
782    CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCC
       GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
                             ^                       ^
       816 BGLI, 833 DRD1,

       ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
842    GTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACT
       CAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGA
                                               ^
       881 SACI,

       ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902    ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
       TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA
                                      ^
       931 SMAI XMAI,

       GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
962    GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG
       CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
                             ^
       985 STUI,

       ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022   ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
       TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
                                                       ^
       1069 DRA3,

       ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
1082   AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG
```

FIG. 21-Page 2

```
                    MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
  2  AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
     TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTG
     ^                        ^                                  ^
     1 HIND3, 24 NDEI, 52 SCAI,


        ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
 62  CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
     GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
                                                            ^
     116 CLAI,


        ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
122  CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
     GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG


        TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
182  TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
     ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACA


        AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
242  GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
     CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT


        AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
302  GCAGAGACTGCGGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
     CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG
        ^
     303 ALWN1,


        ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
362  ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
     TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA


        TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
422  TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT
     ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTA
```

FIG. 22-Page 1

5449 APAI,

```
         GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
5462     GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
         CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
              ^            ^                            ^         ^
         5467 BSSH2, 5478 XMNI, 5502 XHOI,  5511 AAT2,


         IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
5522     ATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
         TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
                                    ^           ^       ^   ^
         5548 ALWN1,  5558 ESP1,  5564 SMAI XMAI,  5568 KPNI,


         LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
5582     CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGG
         GAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC


         ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAsp
5642     CCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGAT
         GGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA
              ^                                                    ^
         5650 APAI,  5696 CLAI,


         ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValOC AM
5702     ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCTAATAGTCGAC
         TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGATTATCAGCTG
                                    ^                           ^
         5724 HGIE2,  5755 SALI,
```

FIG. 21-Page 10

3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC
     GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG
                    ^   ^
     3143 ALWN1, 3164 EAG1 XMA3,

         ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
3182 CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG
     GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC
                                            ^   ^
     3217 HGIE2, 3229 NCOI,

         LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
3242 CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC
     GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG

         ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
     TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
                                       ^   ^
     3332 SACI, 3346 HIND3,

         SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
3362 TCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGC
     AGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCG

         CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
3422 TGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCCTGGAGGGGGAGCCT
     ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
                   ^
     3437 EAM11051,

         GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
3482 GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
     CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
        ^^ ^
     3484 BAMHI, 3485 BSAB1, 3487 BSPE1,

         AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
3542 GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC
     CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG
                                           ^   ^
     3589 DRA3, 3600 SAC2,

         AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
3602 GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT
     CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
               ^   ^
     3611 ALWN1, 3655 PFLM1,

         LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
3662 TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC
     AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
                          ^
     3681 DRA3,

         ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
3722 AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG

FIG. 18-Page 6

```
         ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
2522     CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
         GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
                                      ^
    2553 PSTI,


         ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
2582     GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
         CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
                                      ^
    2594 DRA3,


         ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
2642     GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC
         CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG


         ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
2702     CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
         GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
                                                                  ^
    2757 HGIE2,


         ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762     GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
         CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
                                                                ^
    2809 AAT2,


         ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
2822     ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
         TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
                                          ^
    2850 EAG1 XMA3,


         ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
2882     CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
         GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
                    ^                   ^
    2889 BALI, 2903 NHEI,


         ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
2942     ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
         TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
                                  ^  ^
    2966 ESP1, 2969 SACI,


         GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
3002     GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC
         CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG


         PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
3062     TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG
         AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
                                                  ^
    3096 BGL2,


         ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
```

FIG. 18–Page 5

```
                    MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
  2  AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
     TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTG
     ^                       ^                                   ^
     1 HIND3, 24 NDEI, 52 SCAI,


        ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
 62  CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
     GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
                                                                 ^
     116 CLAI,


        ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
122  CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
     GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG


        TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
182  TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
     ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACA


        AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
242  GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
     CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT


        AlaGluThrAlaGlyAlaAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
302  GCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
     CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG
     ^
     303 ALWN1,


        ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
362  ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
     TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA


        TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
422  TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT
     ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTA
```

FIG. 21-Page 1

```
4862  AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
      TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
                                      ^
      4893 BGL2,


      ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922  CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
      GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
                                     ^
      4954 NCOI,


      SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
4982  AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG
      TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
                                      ^                          ^
      5015 SPHI, 5035 KPNI,


      ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042  CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
      GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
                              ^                          ^
      5064 APAI, 5091 BALI,


      GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102  GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
      CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
                    ^
      5113 NDEI,


      LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
5162  CTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
      GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATG
                     ^^        ^      ^
      5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,


      SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222  AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
      TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
                       ^
      5240 DRA3,


      LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
5282  CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT
      GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
                    ^
      5295 PSTI,


      ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
5342  CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCCGCAGGACGTCAAGTTC
      GGATTTGGAGTTTCTTTCTGGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG
                                              ^^         ^        ^
      5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,


      ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
5402  CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
      GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC
                                                           ^
```

FIG. 21-Page 9

4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
4262 GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG
                                    ^   ^

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG
                        ^

4345 APAI,

TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
4382 TATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG

TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
4442 TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC
                    ^

4452 SMAI XMAI,

CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
            ^ ^

4508 DRD1, 4511 TTH3I,

LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCACAA
GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGGACCCCTGGGGGGTGTT

ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG
                        ^

4637 SACI,

GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT
CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA
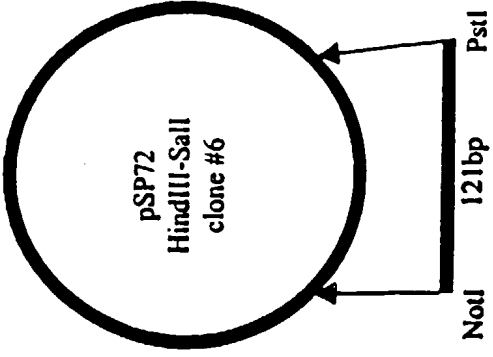   ^

4731 NRUI,

AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
4742 GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA

AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
4802 GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC
CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
        ^^

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

FIG. 21-Page 8

Ligate fragments into pd.NS3NS5.PJ
NotI-SalI cloning vector.

pSP72
HindIII-SalI
clone #6

PstI

121bp

NotI

pd.ΔNS3NS5.PJ
core150RT

SalI

PstI

NotI

pd.ΔNS3NS5.PJ
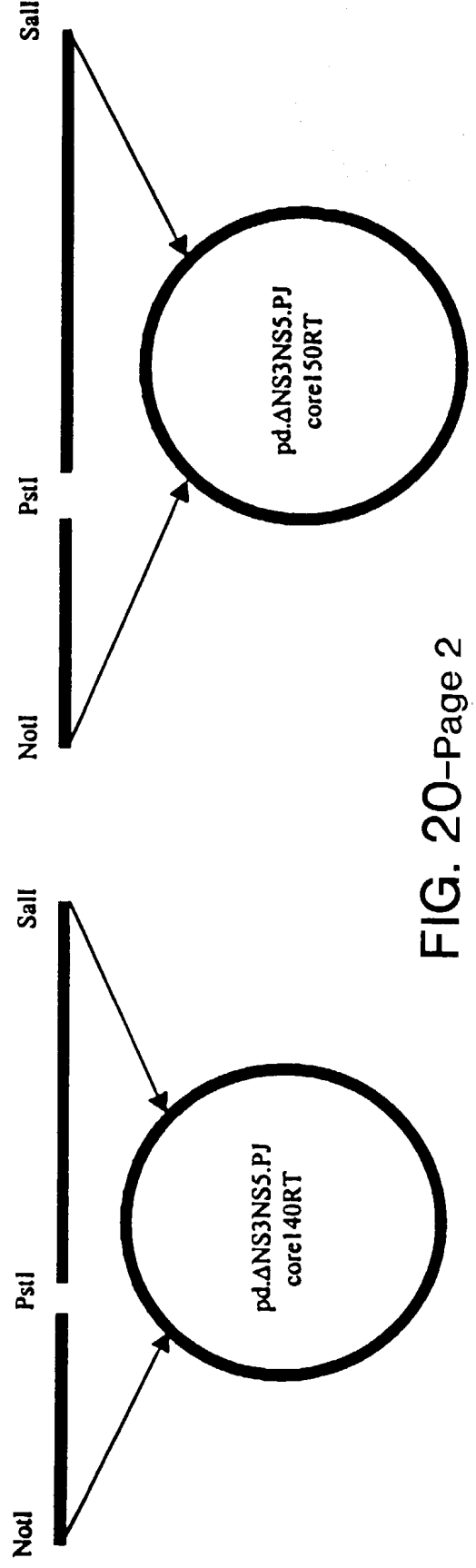core140RT

SalI

PstI

NotI

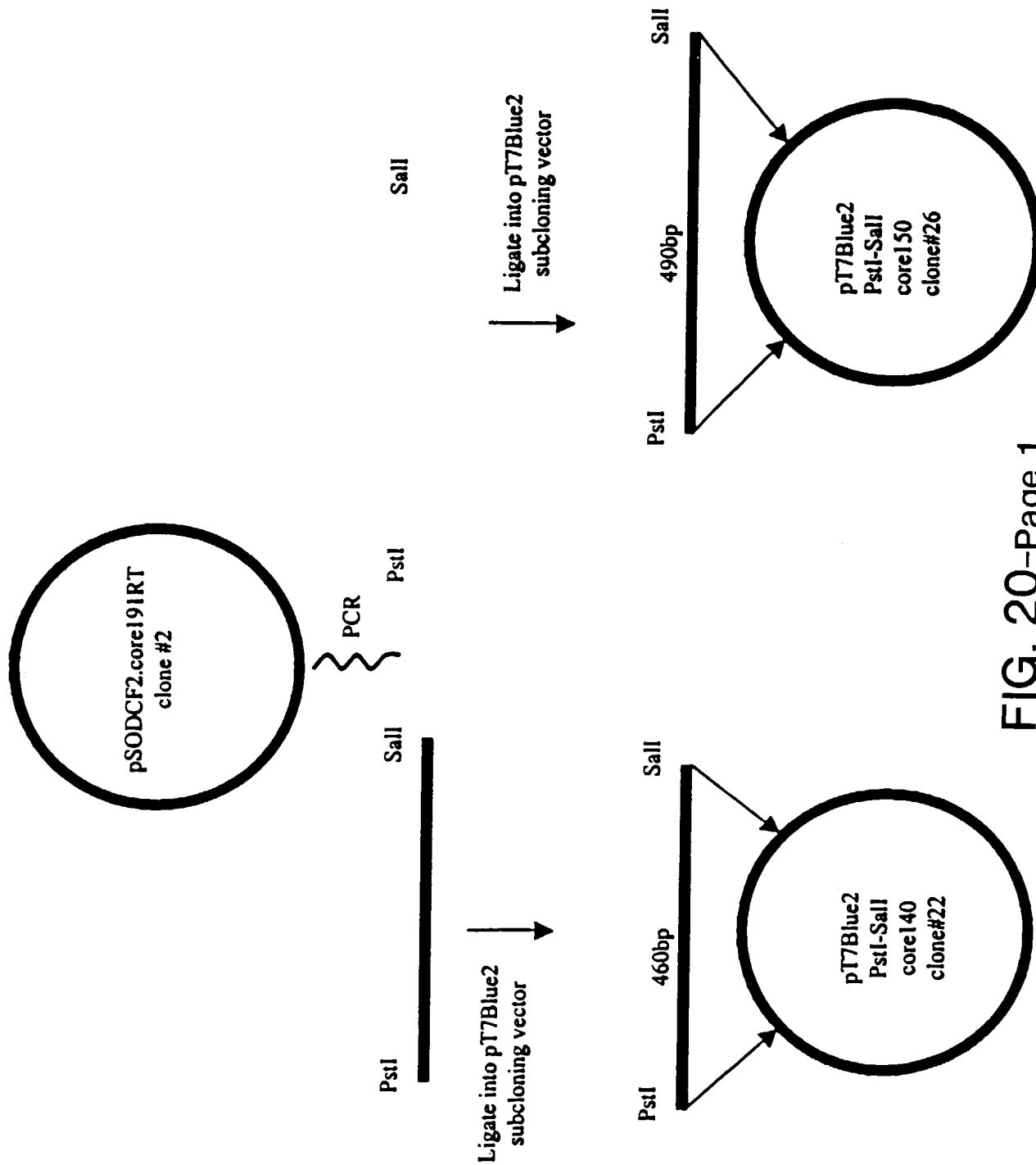FIG. 20-Page 2

FIG. 20-Page 1

```
        ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
1922    ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
        TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
           ^
        1928 TTH3I,


        ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
1982    GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG
        CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCGTCACGTCACC
                            ^                    ^
        2004 NAEI, 2017 SMAI XMAI,


        MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
2042    ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
        TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
                                   ^                        ^
        2067 SMAI XMAI, 2093 DRA3,


        ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
2102    CCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
        GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
                     ^                                            ^
        2115 PVU2, 2159 ALWN1,


        LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
2162    CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC
        GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
            ^                                                      ^
        2164 MST2, 2220 ECON1,


        TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
2222    TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
        ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT


        LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
2282    AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT
        TTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCATA
            ^                        ^          ^
        2285 ESP1, 2300 PVU2, 2310 BAMHI,


        LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
2342    AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC
        TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG


        ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
2402    ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
        TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
                     ^                        ^          ^^
        2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,


        TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
2462    TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG
        ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
                     ^                        ^
        2480 ASE1, 2497 APAI,
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FIG. 18–Page 4

```
              CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC

              SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
        1322  TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
              AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
                                                                         ^
        1369  NAEI,


              ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
        1382  CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
              GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTGAAT
                         ^
        1385  DRD1,


              ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
        1442  CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
              GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG


              LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
        1502  CTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
              GACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT
              ^         ^
        1502  PSTI,  1507 TTH3I,


              LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
        1562  AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
              TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC
              ^                            ^
        1565  XHOI,  1586 NDEI,


              AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
        1622  GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
              CGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
                              ^                                      ^
        1643  BSTE2,  1677 ALWN1 PVU2,


              AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
        1682  GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
              CGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC


              ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
        1742  GTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCT
              CACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGA
                                                                        ^
        1794  ESP1,


              GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
        1802  GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT
              CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA
              ^
        1802  KAS1 NARI,


              GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
        1862  GGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC
              CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
                                 ^                      ^
        1878  SACI,  1899 BSPH1,


                                FIG. 18–Page 3
```

```
          LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
2342  AAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC
      TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG


          ThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
2402  ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
      TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
                              ^                    ^        ^^
      2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,


          TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
2462  TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG
      ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
                          ^                    ^
      2480 ASE1, 2497 APAI,


          ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
2522  CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
      GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
                                            ^
      2553 PSTI,


          ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
2582  GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
      CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
                      ^
      2594 DRA3,


          ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
2642  GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC
      CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG


          ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
2702  CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
      GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
                                                            ^
      2757 HGIE2,


          ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762  GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
      CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
                                                        ^
      2809 AAT2,


          ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
2822  ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
      TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
                              ^
      2850 EAG1 XMA3,


          ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
2882  CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
      GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
                      ^                    ^
      2889 BALI, 2903 NHEI,
```
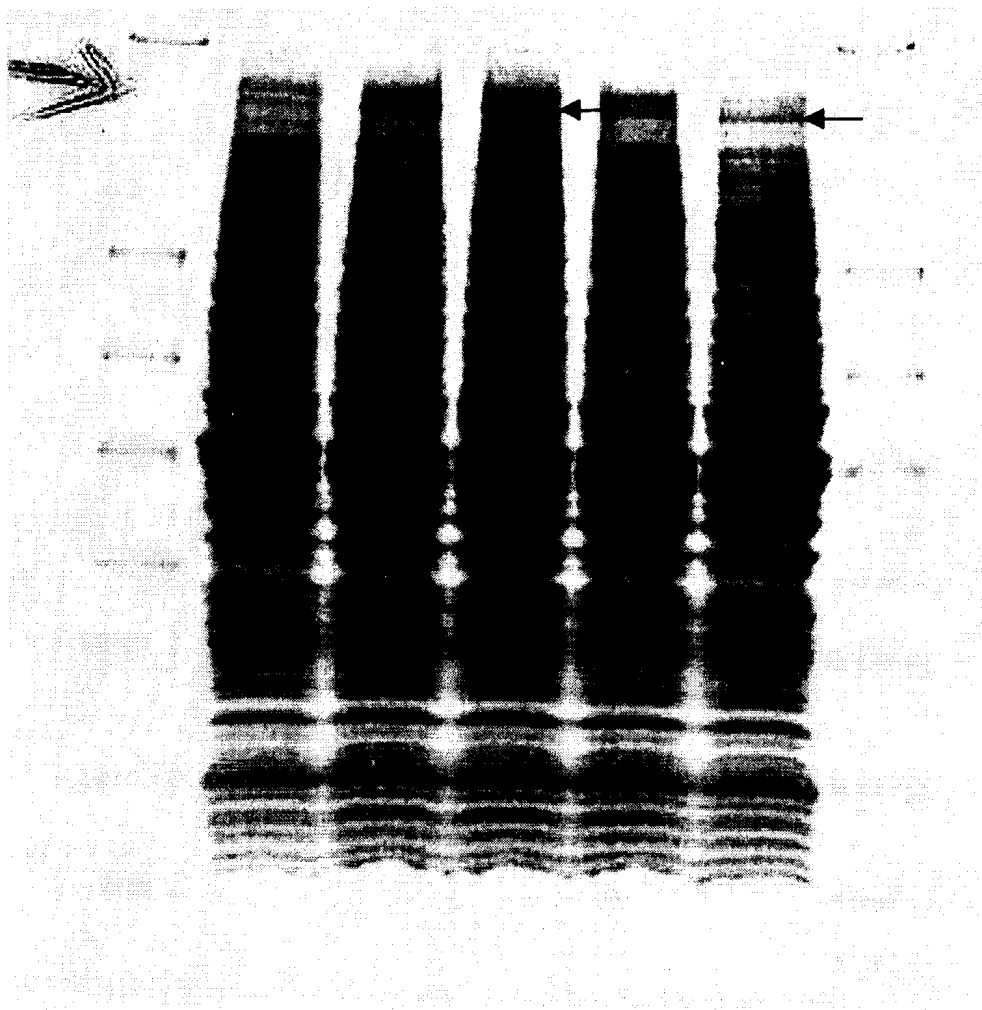
FIG. 17-Page 5

FIG. 19

```
      ValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGlyLeuAla
1742  GTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGCTTAGCT
      CACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCGAATCGA
                                                                 ^
1794  ESP1,


      GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
1802  GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT
      CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA
      ^
1802  KAS1 NARI,


      GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer
1862  GGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC
      CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
                      ^                           ^
1878  SACI, 1899 BSPH1,


      ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
1922  ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
      TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
           ^
1928  TTH3I,


      ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp
1982  GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG
      CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC
                              ^                 ^
2004  NAEI, 2017 SMAI XMAI,


      MetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
2042  ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
      TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
                            ^                             ^
2067  SMAI XMAI, 2093 DRA3,


      ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
2102  CCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
      GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
                  ^                                           ^
2115  PVU2, 2159 ALWN1,


      LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
2162  CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC
      GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
      ^                                                         ^
2164  MST2, 2220 ECON1,


      TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
2222  TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
      ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT


      LysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArgGlyTyr
2282  AAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGCGGGTAT
      TTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCGCCCATA
      ^               ^           ^
2285  ESP1, 2300 PVU2, 2310 BAMHI,
```

FIG. 17-Page 4

```
          TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTC


       ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
1142   CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
       GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
                      ^
       1150 NCOI,


       ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
1202   ACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTC
       TGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG
                                       ^       ^   ^        ^       ^
       1230 BSPH1,  1234 DRD1,  1237 AVA3,  1245 EAG1 XMA3,  1250 DRD1,


       ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
1262   GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG
       CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC


       SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaIleIle
1322   TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
       AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
                                                              ^
       1369 NAEI,


       ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGlnHisLeu
1382   CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
       GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTCGTGAAT
             ^
       1385 DRD1,


       ProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
1442   CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
       GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG


       LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
1502   CTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
       GACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT
       ^       ^
       1502 PSTI,  1507 TTH3I,


       LysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
1562   AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
       TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC
            ^                            ^
       1565 XHOI,  1586 NDEI,


       AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla
1622   GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT
       CGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
                        ^                                           ^
       1643 BSTE2,  1677 ALWN1 PVU2,


       AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
1682   GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
       CGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCCCCCACC
```

FIG. 17–Page 3

```
       ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
  662  ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATC
       TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG


       ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
  722  ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
       TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC


       ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
  782  CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCC
       GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
                                                     ^                    ^

  816 BGLI,  833 DRD1,


       ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
  842  GTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACT
       CAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGA
                                                     ^

  881 SACI,


       ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
  902  ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
       TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA
                                     ^

  931 SMAI XMAI,


       GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
  962  GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG
       CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
                                         ^

  985 STUI,


       ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
 1022  ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
       TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
                                                              ^

 1069 DRA3,


       ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
 1082  AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG
       TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTC


       ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142  CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
       GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
                     ^

 1150 NCOI,


       ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
 1202  ACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTC
       TGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG
                                      ^  ^  ^              ^     ^

 1230 BSPH1,  1234 DRD1,  1237 AVA3,  1245 EAG1 XMA3,  1250 DRD1,


       ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
 1262  GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG
```

FIG. 18–Page 2

```
        ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAsp
5642    CCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGAT
        GGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA
                  ^                                             ^

5650 APAI, 5696 CLAI,


        ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu
5702    ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTT
        TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA
                        ^                             ^       ^

5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,


        GlyGlyAlaAlaArgAlaLeuAlaHisGlyValArgValLeuGluAspGlyValAsnTyr
5762    GGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTAT
        CCTCCGCGACGGTCCCGGGACCGCGTACCGCAGGCCCAAGACCTTCTGCCGCACTTGATA
                  ^  ^

5772 BSTXI, 5775 APAI,


        AlaThrGlyAsnLeuProGlyCysSerOC AM
5822    GCAACAGGGAACCTTCCTGGTTGCTCTTAATAGTCGAC
        CGTTGTCCCTTGGAAGGACCAACGAGAATTATCAGCTG
                                            ^

5854 SALI,
```

FIG. 18–Page 10

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
        ^   ^
5064 APAI, 5091 BALI,

GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
        ^
5113 NDEI,

LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
5162 CTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATG
        ^^   ^   ^
5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
                        ^
5240 DRA3,

LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT
GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
        ^
5295 PSTI,

ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCCGCAGGACGTCAAGTTC
GGATTTGGAGTTTCTTTCTGGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG
                                        ^^   ^   ^
5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,

ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
5402 CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC
                                                  ^
5449 APAI,

GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
5462 GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
        ^   ^   ^   ^
5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
5522 ATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
                                  ^   ^   ^   ^
5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
5582 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGG
GAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

```
                  MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
    2  AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
       TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTG
       ^                     ^                                    ^
    1 HIND3, 24 NDEI, 52 SCAI,


                  ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
   62  CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
       GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
                                                                  ^
  116 CLAI,


                  ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
  122  CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
       GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG


                  TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
  182  TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
       ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACA


                  AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
  242  GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
       CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT


                  AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
  302  GCAGAGACTGCGGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
       CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG
       ^
  303 ALWN1,


                  ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
  362  ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
       TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA


                  TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
  422  TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT
       ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTA


                  SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
  482  TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
       AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC


                  AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
  542  GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG
       CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC
                ^             ^
  550 SAC2, 560 DRD1,


                  AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
  602  GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
       CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
                ^
  615 BSPH1,
```

FIG. 18-Page 1

```
       SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
482    TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
       AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC


       AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
542    GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG
       CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC
                ^              ^
       550 SAC2, 560 DRD1,


       AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
602    GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
       CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
                              ^
       615 BSPH1,


       ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
662    ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATC
       TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG


       ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
722    ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
       TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC


       ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
782    CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCC
       GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
                                   ^                      ^
       816 BGLI, 833 DRD1,


       ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
842    GTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACT
       CAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGA
                                   ^
       881 SACI,


       ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902    ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
       TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA
                                   ^
       931 SMAI XMAI,


       GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
962    GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG
       CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
                              ^
       985 STUI,


       ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022   ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
       TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
                                                          ^
       1069 DRA3,


       ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
1082   AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG
```

FIG. 17-Page 2

```
2522   CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
       GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
                                                    ^
       2553 PSTI,


       ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
2582   GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG
       CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
                          ^
       2594 DRA3,


       ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro
2642   GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC
       CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG


       ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
2702   CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
       GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
                                                               ^
       2757 HGIE2,


       ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762   GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
       CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
                                                         ^
       2809 AAT2,


       ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
2822   ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
       TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
                                        ^
       2850 EAG1 XMA3,


       ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
2882   CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
       GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
           ^                            ^
       2889 BALI, 2903 NHEI,


       ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
2942   ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
       TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
                                    ^   ^
       2966 ESP1, 2969 SACI,


       GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
3002   GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC
       CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG


       PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
3062   TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG
       AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
                                                    ^
       3096 BGL2,


       ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
3122   CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC
```

FIG. 14–Page 5

```
                   MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
  2 AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
    TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTG
    ^                        ^                                  ^
    1 HIND3, 24 NDEI, 52 SCAI,


    ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
 62 CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
    GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
                                                            ^
    116 CLAI,


    ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
122 CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
    GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG


    TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
182 TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
    ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACA


    AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
242 GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
    CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT


    AlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
302 GCAGAGACTGCGGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
    CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG
    ^
    303 ALWN1,


    ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
362 ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
    TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA


    TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
422 TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTCTGTCAT
    ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAGACAGTA
```

FIG. 17-Page 1

TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
4442 TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC
                 ^
4452 SMAI XMAI,

CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
         ^   ^
4508 DRD1, 4511 TTH3I,

LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCACAA
GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTT

ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG
                  ^
4637 SACI,

GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT
CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA
                                                      ^
4731 NRUI,

AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
4742 GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA

AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
.4802 GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC
CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
                 ^^
4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu
4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
                                          ^
4893 BGL2,

ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
                                         ^
4954 NCOI,

SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG
TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
                                ^   ^
5015 SPHI, 5035 KPNI,

FIG. 18-Page 8

5449 APAI,

```
                   GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
5462   GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
                   CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
                   ^                 ^                        ^             ^
```

5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

```
                   IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
5522   ATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
                   TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
                                             ^           ^       ^  ^
```

5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

```
                   LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
5582   CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGG
                   GAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC
```

```
                   ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysOC AM
5642   CCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGTAATAGTCG
                   GGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCATTATCAGC
                   ^                                                           ^
```

5650 APAI, 5698 SALI,

5702 AC
         TG

FIG. 17–Page 10

Ligate fragments into pd.NS3NS5.PJ
NotI-SalI cloning vector.

pSP72
HindIII-SalI
clone #6

Pstl
121bp
Notl

Notl Pstl 403bp Sall

pd.ΔNS3NS5.PJ
core121RT

NotI 559bp PstI SalI

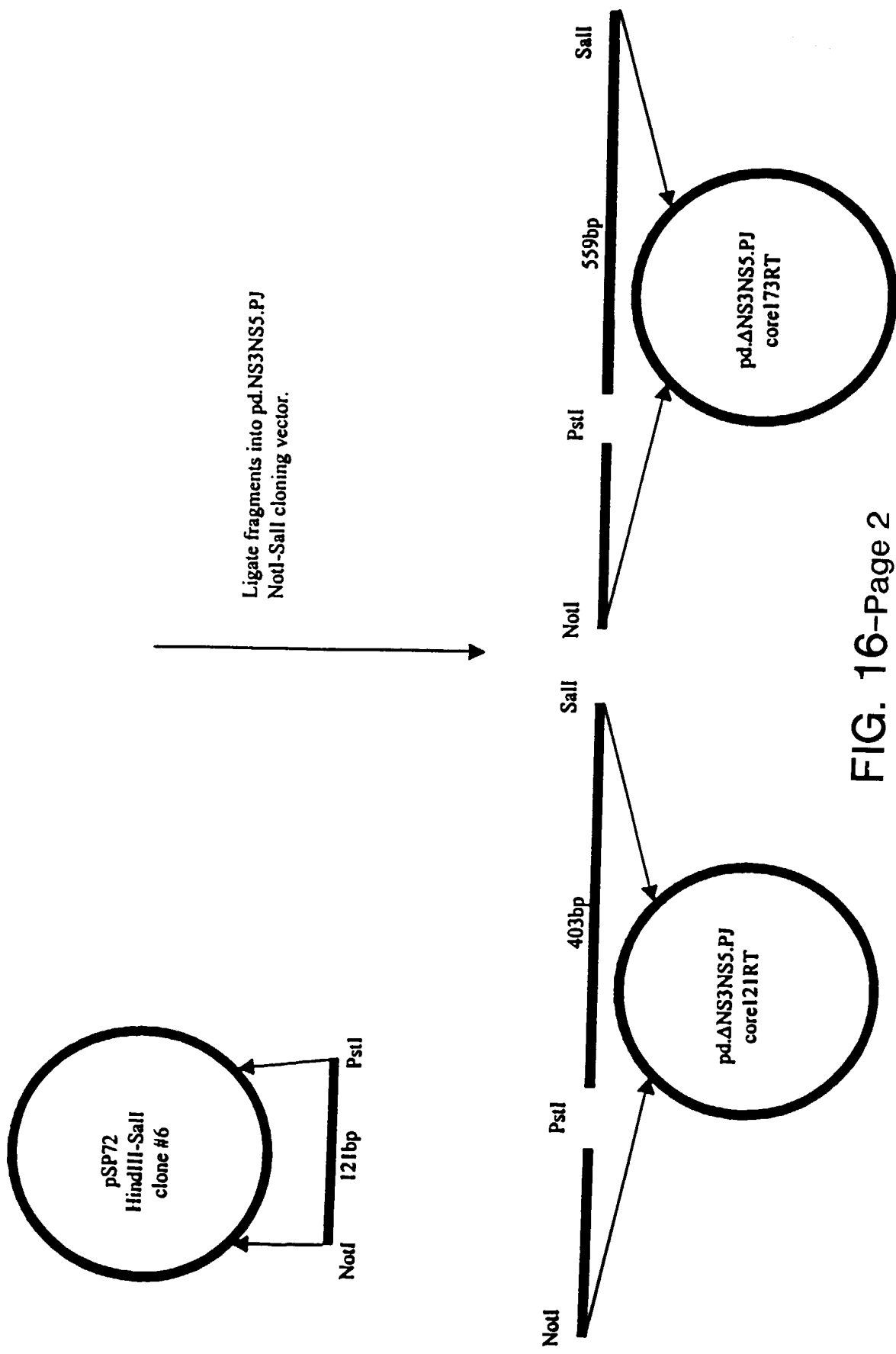pd.ΔNS3NS5.PJ
core173RT

FIG. 16–Page 2

4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
     TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
                              ^
     4893 BGL2,

     ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
     GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
                                       ^
     4954 NCOI,

     SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
4982 AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG
     TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
                                     ^   ^
     5015 SPHI, 5035 KPNI,

     ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
     GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
                              ^   ^
     5064 APAI, 5091 BALI,

     GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
     CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
                       ^
     5113 NDEI,

     LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
5162 CTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
     GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATG
                         ^^   ^   ^
     5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

     SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222 AGCGGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
     TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
                      ^
     5240 DRA3,

     LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgMetSerThrAsn
5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT
     GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
                      ^
     5295 PSTI,

     ProLysProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspValLysPhe
5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGCGGCCGCAGGACGTCAAGTTC
     GGATTTGGAGTTTCTTTCTGGTTTGCATTGTGGTTGGCCGCCGGCGTCCTGCAGTTCAAG
                                     ^^   ^   ^
     5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,

     ProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
5402 CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
     GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC
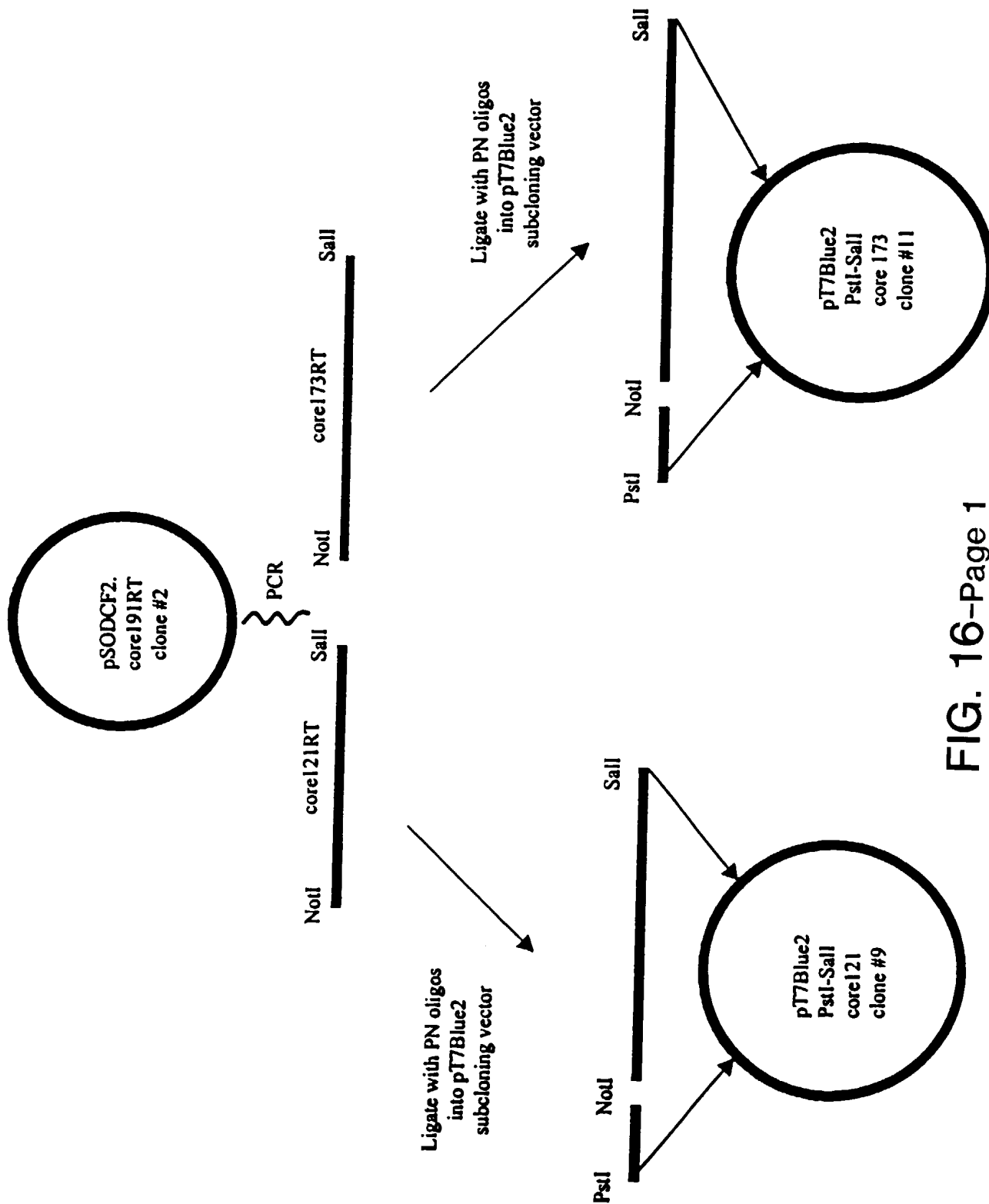   ^
                    FIG. 17-Page 9

FIG. 16–Page 1

4229 DRD1, 4236 ALWN1,

```
      GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
4262  GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
      CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG
                                                ^         ^
```

4301 BGLI, 4308 BALI,

```
      LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322  CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
      GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG
                          ^
```

4345 APAI,

```
      TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
4382  TATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
      ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG
```

```
      TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
4442  TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
      ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC
                        ^
```

4452 SMAI XMAI,

```
      CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502  TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
      ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
                      ^   ^
```

4508 DRD1, 4511 TTH3I,

```
      LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
4562  CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCACAA
      GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTT
```

```
      ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
4622  CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
      GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG
                                  ^
```

4637 SACI,

```
      GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
4682  GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT
      CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA
                                                          ^
```

4731 NRUI,

```
      AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
4742  GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
      CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
```

```
      AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
4802  GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC
      CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
                ^^
```

4806 PFLM1, 4807 DRA3,

```
      ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu
```

FIG. 17-Page 8

3589 DRA3, 3600 SAC2,

```
      AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
3602  GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT
      CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
         ^                                                     ^
```

3611 ALWN1, 3655 PFLM1,

```
      LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
3662  TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC
      AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
                                      ^
```

3681 DRA3,

```
      ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
3722  AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG
      TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
```

```
      SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
3782  TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC
      AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
                                              ^
```

3816 HIND3,

```
      SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
3842  TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
      AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
                                            ^                 ^
```

3875 AAT2, 3890 BGLI,

```
      ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
3902  GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
      CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
```

```
      ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
3962  ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG
      TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
```

```
      ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
4022  CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG
      GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
```

```
      TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
4082  TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
      ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
```

```
      SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
4142  TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
      AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
                                   ^
```

4160 ECORI,

```
      GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
4202  GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
      CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC
                                        ^          ^
```

FIG. 17-Page 7

```
           ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
   2942    ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
           TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC
                                         ^   ^
           2966 ESP1, 2969 SACI,


           GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
   3002    GAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC
           CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG


           PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
   3062    TTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAAATCCTG
           AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
                                                    ^
           3096 BGL2,


           ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro
   3122    CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC
           GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG
                                ^                           ^
           3143 ALWN1, 3164 EAG1 XMA3,


           ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
   3182    CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG
           GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC
                                              ^                ^
           3217 HGIE2, 3229 NCOI,


           LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
   3242    CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC
           GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG


           ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
   3302    ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
           TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
                                              ^                 ^
           3332 SACI, 3346 HIND3,


           SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
   3362    TCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGC
           AGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCG


           CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
   3422    TGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCT
           ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
                          ^
           3437 EAM11051,


           GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
   3482    GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
           CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
                  ^^ ^
           3484 BAMHI, 3485 BSAB1, 3487 BSPE1,


           AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
   3542    GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC
           CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG
```

FIG. 17–Page 6

FIG. 15

662 ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAGACAATC
    TGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTCTGTTAG

    ThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
722 ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
    TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC

    ProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAspSerSer
782 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCC
    GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG
                                      ^   ^
816 BGLI, 833 DRD1,

    ValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAlaGluThr
842 GTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCCGAGACT
    CAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGGCTCTGA
                                                  ^
881 SACI,

    ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGACCATCTT
    TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA
                                  ^
931 SMAI XMAI,

    GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln
962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG
    CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC
                                ^
985 STUI,

    ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla
1022 ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT
     TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA
                                                 ^
1069 DRA3,

    ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
1082 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG
     TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTC

    ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
1142 CCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
     GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
                    ^
1150 NCOI,

    ThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeuGluVal
1202 ACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTGGAGGTC
     TGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGACCTCCAG
                                       ^ ^ ^   ^   ^
1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,

    ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu
1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG
     CAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATAACGGAC

FIG. 14-Page 2

5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCCAGAGGA
     GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT
                        ^   ^
5064 APAI, 5091 BALI,

     GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
     CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
                   ^
5113 NDEI,

     LeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAlaGlyTyr
5162 CTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTAC
     GAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGACCGATG
                  ^^   ^   ^
5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

     SerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
     TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACCAAAACG
                      ^
5240 DRA3,

     LeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgOP
5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGATGAATAGTCGAC
     GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTACTTATCAGCTG
     ^^
5295 PSTI, 5336 SALI,

FIG. 14-Page 9

```
        TyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
4442    TACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
        ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTACGAGCAC
                      ^
        4452 SMAI XMAI,


        CysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502    TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGGTCCAGGAGGACGCGGCGAGC
        ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
             ^    ^
        4508 DRD1, 4511 TTH3I,


        LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
4562    CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCCCCACAA
        GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTT


        ProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
4622    CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
        GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG
                               ^
        4637 SACI,


        GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
4682    GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT
        CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGCTCTCGA
                                                              ^
        4731 NRUI,


        AlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe
4742    GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT
        CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA


        AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla
4802    GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC
        CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG
               ^^
        4806 PFLM1, 4807 DRA3,


        ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu
4862    AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
        TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
                                              ^
        4893 BGL2,


        ProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922    CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
        GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
                                          ^
        4954 NCOI,


        SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro
4982    AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG
        TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC
                                         ^                      ^
        5015 SPHI, 5035 KPNI,


        ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
```

FIG. 14-Page 8

1884 SACI, 1905 BSPH1,

```
      ProSerThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuVal
1922  CCCTCCACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTA
      GGGAGGTGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCAT
                       ^
```

1934 TTH3I,

```
      ValGlyValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaVal
1982  GTCGGCGTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTG
      CAGCCGCACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCAC
                                   ^                 ^
```

2010 NAEI, 2023 SMAI XMAI,

```
      GlnTrpMetAsnArgLeuIleAlaPheAlaSerArgGlyAsnHisValSerProThrHis
2042  CAGTGGATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCAC
      GTCACCTACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTG
                                       ^                         ^
```

2073 SMAI XMAI, 2099 DRA3,

```
      TyrValProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrVal
2102  TACGTGCCGGAGAGCGATGCAGCTGCCCGCGTCACTGCCATACTCAGCAGCCTCACTGTA
      ATGCACGGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACAT
                                   ^
```

2121 PVU2,

```
      ThrGlnLeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSer
2162  ACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCC
      TGGGTCGAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGG
            ^     ^
```

2165 ALWN1, 2170 MST2,

```
      GlySerTrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThr
2222  GGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACC
      CCAAGGACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGG
                ^
```

2226 ECON1,

```
      TrpLeuLysAlaLysLeuMetProGlnLeuProGlyIleProPheValSerCysGlnArg
2282  TGGCTAAAAGCTAAGCTCATGCCACAGCTGCCTGGGATCCCCTTTGTGTCCTGCCAGCGC
      ACCGATTTTCGATTCGAGTACGGTGTCGACGGACCCTAGGGGAAACACAGGACGGTCGCG
                  ^                       ^             ^
```

2291 ESP1, 2306 PVU2, 2316 BAMHI,

```
      GlyTyrLysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAla
2342  GGGTATAAGGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCT
      CCCATATTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGA
```

```
      GluIleThrGlyHisValLysAsnGlyThrMetArgIleValGlyProArgThrCysArg
2402  GAGATCACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGG
      CTCTAGTGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCC
                                   ^                 ^         ^^
```

2431 BSAB1, 2447 AVR2, 2454 SSE83871, 2455 PSTI,

```
      AsnMetTrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeu
2462  AACATGTGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTT
      TTGTACACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAA
```

<p style="text-align:center">FIG. 11-Page 4</p>

```
                       MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuValLeuAsn
   2  AGCTTACAAAACAAAATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTACTCAAC
      TCGAATGTTTTGTTTTACCGACGTATACGTCGAGTCCCGATATTCCACGATCATGAGTTG
      ^                        ^                               ^
      1 HIND3, 24 NDEI, 52 SCAI,


         ProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGlyIleAsp
  62  CCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGGATCGAT
      GGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCCTAGCTA
                                                               ^
      116 CLAI,


         ProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyrSerThr
 122  CCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTACTCCACC
      GGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATGAGGTGG


         TyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIleIleCys
 182  TACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATAATTTGT
      ATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCCGCGAATACTGTATTATTAAACA


         AspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeuAspGln
 242  GACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTTGACCAA
      CTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAACTGGTT


         AlaGluThrAlaGlyAlaAlaArgLeuValValLeuAlaThrAlaThrProProGlySerVal
 302  GCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGCTCCGTC
      CGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCGAGGCAG
      ^
      303 ALWN1,


         ThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIleProPhe
 362  ACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTT
      TGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAGGGAAAA


         TyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePheCysHis
 422  TACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGGAGACATCTCATCTTCTGTCAT
      ATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCCTCTGTAGAGTAGAAGACAGTA


         SerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsnAlaVal
 482  TCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAATGCCGTG
      AGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTACGGCAC


         AlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValValValVal
 542  GCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTCGTCGTG
      CGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAGCAGCAC
                    ^              ^
      550 SAC2, 560 DRD1,


         AlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAspCysAsn
 602  GCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGACTGCAAT
      CGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTGACGTTA
                 ^
      615 BSPH1,


      ThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGluThrIle
```

FIG. 14-Page 1

```
       CysLeuSerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAla
1322   TGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCA
       ACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGT
                                                                  ^
       1375 NAEI,


       IleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGln
1382   ATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAG
       TAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTACCTTCTCACGAGAGTC
                        ^
       1391 DRD1,


       HisLeuProTyrIleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeu
1442   CACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTC
       GTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAG


       GlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsn
1502   GGCCTCCTGCAGACCGCGTCCCGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAAC
       CCGGAGGACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTG
                        ^         ^
       1508 PSTI,  1513 TTH3I,


       TrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGln
1562   TGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAA
       ACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTT
                        ^                        ^
       1571 XHOI,  1592 NDEI,


       TyrLeuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPhe
1622   TACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTT
       ATGAACCGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAA
                                  ^
       1649 BSTE2,


       ThrAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGly
1682   ACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGG
       TGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCC
         ^
       1683 ALWN1 PVU2,


       GlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGly
1742   GGGTGGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGC
       CCCACCCACCGACGGGTCGAGCGGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCG
                                                                  ^
       1800 ESP1,


       LeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAla
1802   TTAGCTGGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCA
       AATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGT
               ^
       1808 KAS1 NARI,


       GlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluVal
1862   GGGTATGGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTC
       CCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAG
                        ^                        ^
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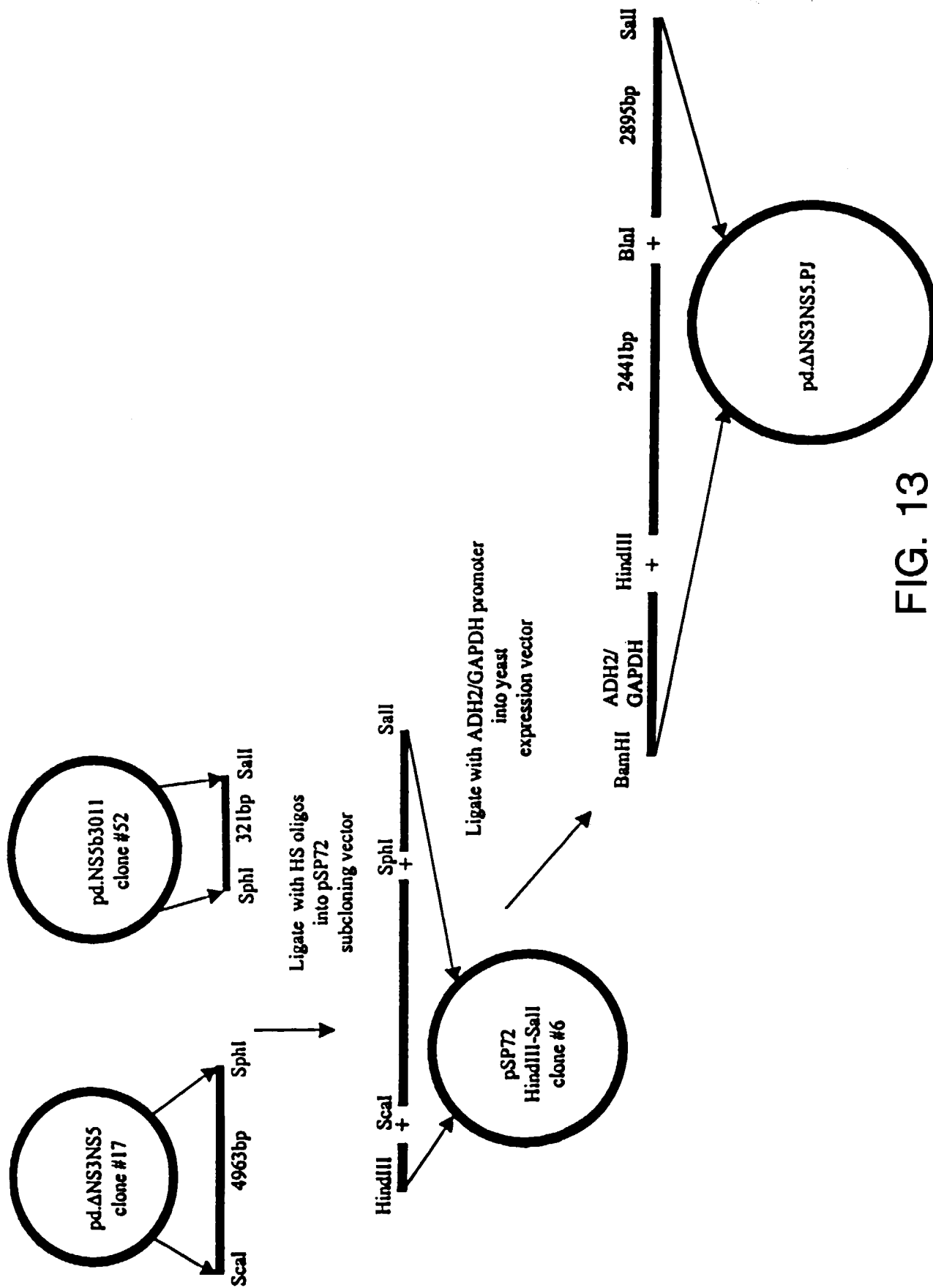
FIG. 11-Page 3

FIG. 13

```
662   TGCAATACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAG
      ACGTTATGCACACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTC


      ThrIleThrLeuProGlnAspAlaValSerArgThrGlnArgArgGlyArgThrGlyArg
722   ACAATCACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGG
      TGTTAGTGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCC


      GlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAsp
782   GGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGAC
      CCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTG
                                            ^                       ^

822   BGLI,  839 DRD1,


      SerSerValLeuCysGluCysTyrAspAlaGlyCysAlaTrpTyrGluLeuThrProAla
842   TCGTCCGTCCTCTGTGAGTGCTATGACGCAGGCTGTGCTTGGTATGAGCTCACGCCCGCC
      AGCAGGCAGGAGACACTCACGATACTGCGTCCGACACGAACCATACTCGAGTGCGGGCGG
                                                            ^

887   SACI,


      GluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAsp
902   GAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGAC
      CTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTG
                                            ^

937   SMAI XMAI,


      HisLeuGluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeu
962   CATCTTGAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTA
      GTAGAACTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGAT
                                            ^

991   STUI,


      SerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrVal
1022  TCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTG
      AGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCAC
                                                            ^

1075  DRA3,


      CysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArg
1082  TGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGC
      ACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCG


      LeuLysProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsn
1142  CTCAAGCCCACCCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAAT
      GAGTTCGGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTA
                             ^

1156  NCOI,


      GluIleThrLeuThrHisProValThrLysTyrIleMetThrCysMetSerAlaAspLeu
1202  GAAATCACCCTGACGCACCCAGTCACCAAATACATCATGACATGCATGTCGGCCGACCTG
      CTTTAGTGGGACTGCGTGGGTCAGTGGTTTATGTAGTACTGTACGTACAGCCGGCTGGAC
                                        ^   ^ ^         ^       ^

1236  BSPH1,  1240 DRD1,  1243 AVA3,  1251 EAG1 XMA3,  1256 DRD1,


      GluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyr
1262  GAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTAT
      CTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATA
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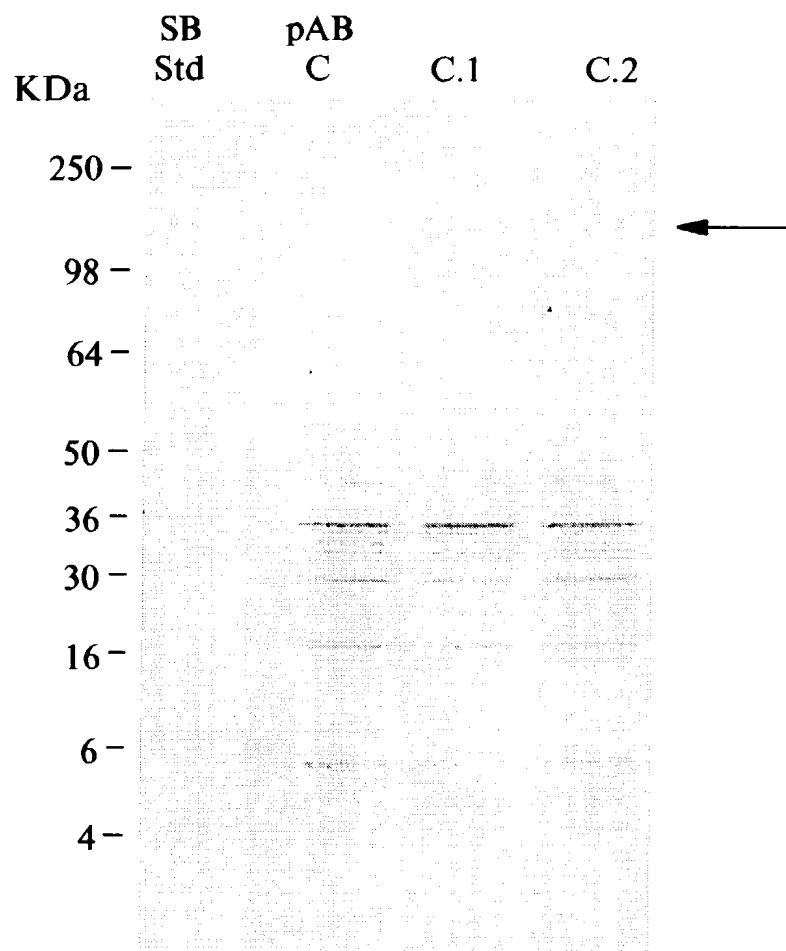
FIG. 11-Page 2

FIG. 12

```
        SerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrProProHis
3782    TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC
        AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
                                                 ^
3816 HIND3,

        SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla
3842    TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC
        AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
                                           ^                  ^
3875 AAT2, 3890 BGLI,

        ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp
3902    GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC
        CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG

        ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys
3962    ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG
        TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC

        ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu
4022    CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG
        GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC

        TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr
4082    TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC
        ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG

        SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet
4142    TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG
        AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
                            ^
4160 ECORI,

        GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr
4202    GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG
        CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC
                                           ^       ^
4229 DRD1, 4236 ALWN1,

        GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer
4262    GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC
        CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG
                                              ^             ^
4301 BGLI, 4308 BALI,

        LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322    CTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
        GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTGACGCCG
                                       ^
4345 APAI,

        TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
4382    TATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC
        ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG
```

<center>

FIG. 14–Page 7

</center>

```
        GCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATATTGGGG
                         ^                          ^
        3143 ALWN1, 3164 EAG1 XMA3,


             ProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGlyCysPro
        3182 CCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGCTGCCCG
             GGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCGACGGGC
                                                  ^              ^
        3217 HGIE2, 3229 NCOI,


             LeuProProProLysSerProProValProProProArgLysLysArgThrValValLeu
        3242 CTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTGGTCCTC
             GAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCACCAGGAG


             ThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGlySerSer
        3302 ACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGCAGCTCC
             TGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCGTCGAGG
                                            ^              ^
        3332 SACI, 3346 HIND3,


             SerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaProSerGly
        3362 TCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGC
             AGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGAAGACCG


             CysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGlyGluPro
        3422 TGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGGGAGCCT
             ACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCCCTCGGA
                             ^
        3437 EAM11051,


             GlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsnAlaGlu
        3482 GGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAACGCGGAG
             CCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTGCGCCTC
                     ^^  ^
        3484 BAMHI, 3485 BSAB1, 3487 BSPE1,


             AspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrProCysAla
        3542 GATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCGTGCGCC
             CTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGCACGCGG
                                                  ^              ^
        3589 DRA3, 3600 SAC2,


             AlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHisHisAsn
        3602 GCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCACCACAAT
             CGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTGGTGTTA
                     ^                                          ^
        3611 ALWN1, 3655 PFLM1,


             LeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThrPheAsp
        3662 TTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACATTTGAC
             AACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGTAAACTG
                             ^
        3681 DRA3,


             ArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAlaAlaAla
        3722 AGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCAGCGGCG
             TCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGTCGCCGC
```

FIG. 14-Page 6

```
           ValProProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAla
5042       GTACCGCCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGGCC
           CATGGCGGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGG
                                       ^                           ^
           5070 APAI,  5097 BALI,


           ArgGlyGlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLys
5102       AGAGGAGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAG
           TCTCCTCCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTC
                                 ^
           5119 NDEI,


           LeuLysLeuThrProIleAlaAlaAlaGlyGlnLeuAspLeuSerGlyTrpPheThrAla
5162       CTCAAACTCACTCCAATAGCGGCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCT
           GAGTTTGAGTGAGGTTATCGCCGGCGACCGGTCGACCTGAACAGGCCGACCAAGTGCCGA
                                 ^^         ^     ^
           5180 NOTI,  5181 EAG1 XMA3,  5188 BALI,  5192 PVU2,


           GlyTyrSerGlyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrp
5222       GGCTACAGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGG
           CCGATGTCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGGCGACCTAGACC
                                         ^
           5246 DRA3,


           PheCysLeuLeuLeuLeuAlaAlaGlyValGlyIleTyrLeuLeuProAsnArgOP
5282       TTTTGCCTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGATGAAGG
           AAAACGGATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTACTTCC
                                 ^                              ^
           5301 PSTI,  5331 HGIE2,


5342       TTGGGGTAAACACTCCGGCCTAAAAAAAAAAAAAAAATCTAGAACCCGAGTCGAC
           AACCCCATTTGTGAGGCCGGATTTTTTTTTTTTTTTAGATCTTGGGCTCAGCTG
                                              ^            ^
           5378 XBAI,  5390 SALI,
```

FIG. 11-Page 9

```
                             MetAlaAlaTyrAlaAlaGlnGlyTyrLysValLeuVal
  2  AGCTTACAAAACAAATTCACCATGGCTGCATATGCAGCTCAGGGCTATAAGGTGCTAGTA
     TCGAATGTTTTGTTTAAGTGGTACCGACGTATACGTCGAGTCCCGATATTCCACGATCAT
     ^                        ^          ^                        ^
     1 HIND3, 21 NCOI, 30 NDEI, 58 SCAI,


                     LeuAsnProSerValAlaAlaThrLeuGlyPheGlyAlaTyrMetSerLysAlaHisGly
 62  CTCAACCCCTCTGTTGCTGCAACACTGGGCTTTGGTGCTTACATGTCCAAGGCTCATGGG
     GAGTTGGGGAGACAACGACGTTGTGACCCGAAACCACGAATGTACAGGTTCCGAGTACCC


                     IleAspProAsnIleArgThrGlyValArgThrIleThrThrGlySerProIleThrTyr
122  ATCGATCCTAACATCAGGACCGGGGTGAGAACAATTACCACTGGCAGCCCCATCACGTAC
     TAGCTAGGATTGTAGTCCTGGCCCCACTCTTGTTAATGGTGACCGTCGGGGTAGTGCATG
     ^
     122 CLAI,


                     SerThrTyrGlyLysPheLeuAlaAspGlyGlyCysSerGlyGlyAlaTyrAspIleIle
182  TCCACCTACGGCAAGTTCCTTGCCGACGGCGGGTGCTCGGGGGGCGCTTATGACATAATA
     AGGTGGATGCCGTTCAAGGAACGGCTGCCGCCCACGAGCCCCCGCGAATACTGTATTAT


                     IleCysAspGluCysHisSerThrAspAlaThrSerIleLeuGlyIleGlyThrValLeu
242  ATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATTGGCACTGTCCTT
     TAAACACTGCTCACGGTGAGGTGCCTACGGTGTAGGTAGAACCCGTAACCGTGACAGGAA


                     AspGlnAlaGluThrAlaGlyAlaArgLeuValValLeuAlaThrAlaThrProProGly
302  GACCAAGCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACCGCCACCCCTCCGGGC
     CTGGTTCGTCTCTGACGCCCCCGCTCTGACCAACACGAGCGGTGGCGGTGGGGAGGCCCG
                     ^
     309 ALWN1,


                     SerValThrValProHisProAsnIleGluGluValAlaLeuSerThrThrGlyGluIle
362  TCCGTCACTGTGCCCCATCCCAACATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATC
     AGGCAGTGACACGGGGTAGGGTTGTAGCTCCTCCAACGAGACAGGTGGTGGCCTCTCTAG


                     ProPheTyrGlyLysAlaIleProLeuGluValIleLysGlyGlyArgHisLeuIlePhe
422  CCTTTTTACGGCAAGGCTATCCCCCTCGAAGTAATCAAGGGGGGGAGACATCTCATCTTC
     GGAAAAATGCCGTTCCGATAGGGGGAGCTTCATTAGTTCCCCCCCTCTGTAGAGTAGAAG


                     CysHisSerLysLysLysCysAspGluLeuAlaAlaLysLeuValAlaLeuGlyIleAsn
482  TGTCATTCAAAGAAGAAGTGCGACGAACTCGCCGCAAAGCTGGTCGCATTGGGCATCAAT
     ACAGTAAGTTTCTTCTTCACGCTGCTTGAGCGGCGTTTCGACCAGCGTAACCCGTAGTTA


                     AlaValAlaTyrTyrArgGlyLeuAspValSerValIleProThrSerGlyAspValVal
542  GCCGTGGCCTACTACCGCGGTCTTGACGTGTCCGTCATCCCGACCAGCGGCGATGTTGTC
     CGGCACCGGATGATGGCGCCAGAACTGCACAGGCAGTAGGGCTGGTCGCCGCTACAACAG
                     ^                    ^
     556 SAC2, 566 DRD1,


                     ValValAlaThrAspAlaLeuMetThrGlyTyrThrGlyAspPheAspSerValIleAsp
602  GTCGTGGCAACCGATGCCCTCATGACCGGCTATACCGGCGACTTCGACTCGGTGATAGAC
     CAGCACCGTTGGCTACGGGAGTACTGGCCGATATGGCCGCTGAAGCTGAGCCACTATCTG
                     ^
     621 BSPH1,


     CysAsnThrCysValThrGlnThrValAspPheSerLeuAspProThrPheThrIleGlu
```

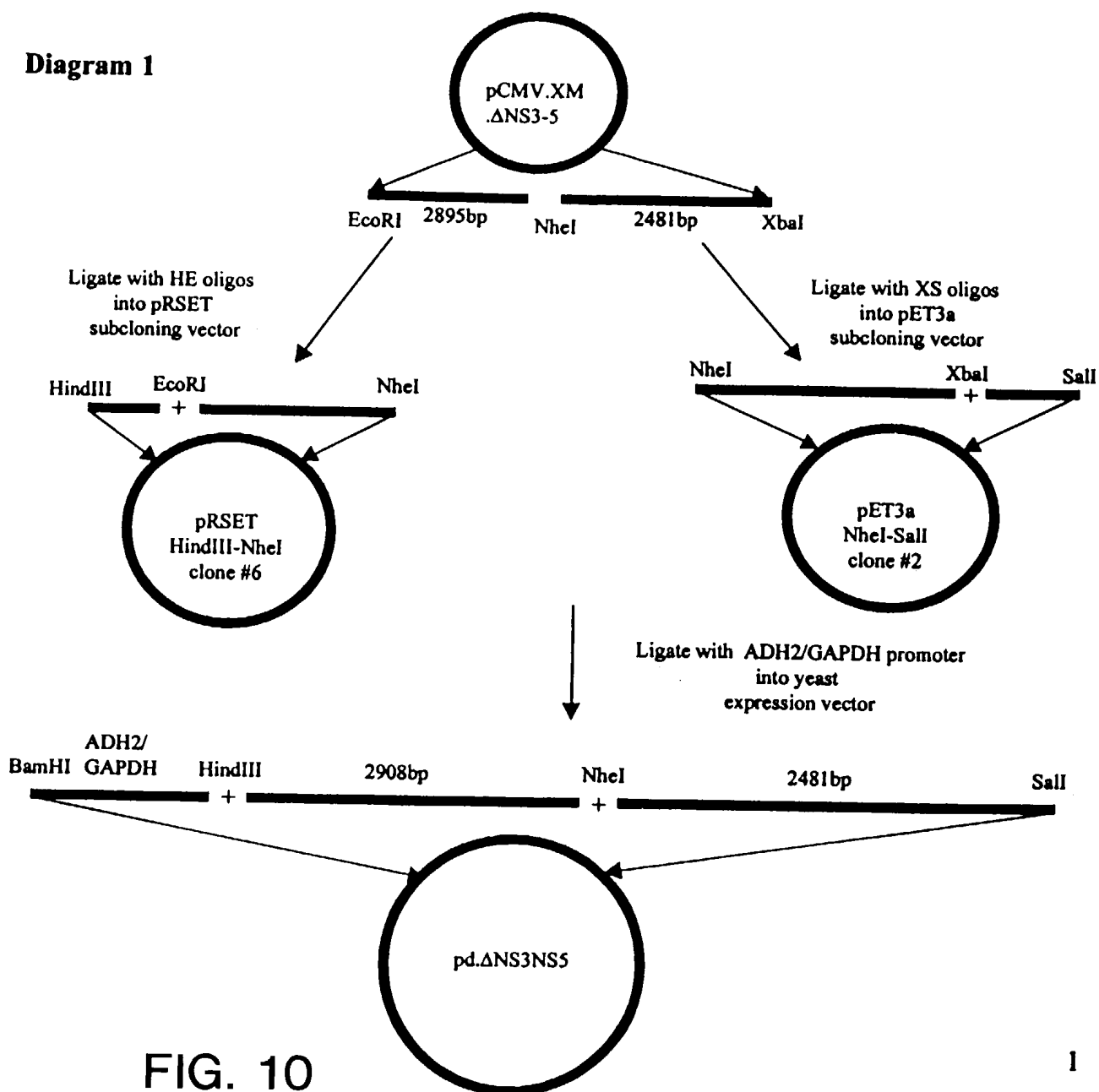# FIG. 11-Page 1

Diagram 1

FIG. 10

1

ACGCCGATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAG

```
           ThrCysTyrIleLysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMet
    4442   ACTTGCTACATCAAGGCCCGGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACCATG
           TGAACGATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGGTAC
                             ^
    4458 SMAI XMAI,
```

```
           LeuValCysGlyAspAspLeuValValIleCysGluSerAlaGlyValGlnGluAspAla
    4502   CTCGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCG
           GAGCACACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGC
                            ^   ^
    4514 DRD1, 4517 TTH3I,
```

```
           AlaSerLeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspPro
    4562   GCGAGCCTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCCTGGGGACCCC
           CGCTCGGACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGG
```

```
           ProGlnProGluTyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAla
    4622   CCACAACCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCC
           GGTGTTGGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGG
                                    ^
    4643 SACI,
```

```
           HisAspGlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAla
    4682   CACGACGGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCG
           GTGCTGCCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGAGCGC
                                                                     ^
    4737 NRUI,
```

```
           ArgAlaAlaTrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIle
    4742   AGAGCTGCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATC
           TCTCGACGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAG
```

```
           MetPheAlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeu
    4802   ATGTTTGCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTT
           TACAAACGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAA
                         ^^
    4812 PFLM1, 4813 DRA3,
```

```
           IleAlaArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSer
    4862   ATAGCCAGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGCCTGCTACTCC
           TATCGGTCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGG
                                                                 ^
    4899 BGL2,
```

```
           IleGluProLeuAspLeuProProIleIleGlnArgLeuHisGlyLeuSerAlaPheSer
    4922   ATAGAACCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCA
           TATCTTGGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGT
                                                    ^
    4960 NCOI,
```

```
           LeuHisSerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGly
    4982   CTCCACAGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGG
           GAGGTGTCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCC
                                                      ^                ^
    5021 SPHI, 5041 KPNI,
```

FIG. 11-Page 8

3722 TTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCA
AAACTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGT

        AlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrPro
3782 GCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCC
CGCCGCAGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGG
                                       ^

3822 HIND3,

        ProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArg
3842 CCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGA
GGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCT
                                 ^   ^

3881 AAT2, 3896 BGLI,

        LysAlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrPro
3902 AAGGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCA
TTCCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGT

        IleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGly
3962 ATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGT
TATCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCA

        ArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMet
4022 CGTAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATG
GCATTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTAC

        AlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPhe
4082 GCTTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTC
CGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAG

        GlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThr
4142 CAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACC
GTTATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGG
                                 ^

4166 ECORI,

        ProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIle
4202 CCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATC
GGTTACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAG
                                    ^   ^

4235 DRD1, 4242 ALWN1,

        ArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIle
4262 CGTACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATC
GCATGCCTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAG
                                             ^   ^

4307 BGLI, 4314 BALI,

        LysSerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsn
4322 AAGTCCCTCACCGAGAGGCTTTATGTTGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAC
TTCAGGGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTG
                                             ^

4351 APAI,

        CysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeu
4382 TGCGGCTATCGCAGGTGCCGCGCGAGCGGCGTACTGACAACTAGCTGTGGTAACACCCTC

FIG. 11–Page 7

```
      IleLeuArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyr
3122  ATCCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTAT
      TAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGGACGGGCAAACCCGCGCCGGCCTGATA
                          ^                                  ^
3149 ALWN1, 3170 EAG1 XMA3,


      AsnProProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGly
3182  AACCCCCCGCTAGTGGAGACGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGC
      TTGGGGGGCGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCG
                                               ^                 ^
3223 HGIE2, 3235 NCOI,


      CysProLeuProProProLysSerProProValProProProArgLysLysArgThrVal
3242  TGCCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTG
      ACGGGCGAAGGTGGAGGTTTCAGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCAC


      ValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGly
3302  GTCCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCACCAGAAGCTTTGGC
      CAGGAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCG
                                    ^                   ^
3338 SACI, 3352 HIND3,


      SerSerSerThrSerGlyIleThrGlyAspAsnThrThrThrSerSerGluProAlaPro
3362  AGCTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCT
      TCGAGGAGTTGAAGGCCGTAATGCCCGCTGTTATGCTGTTGTAGGAGACTCGGGCGGGGA


      SerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGly
3422  TCTGGCTGCCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGG
      AGACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCC
                        ^
3443 EAM11051,


      GluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsn
3482  GAGCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAAC
      CTCGGACCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTG
                    ^^ ^
3490 BAMHI, 3491 BSAB1, 3493 BSPE1,


      AlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrPro
3542  GCGGAGGATGTCGTGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCG
      CGCCTCCTACAGCACACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGC
                                                        ^
3595 DRA3,


      CysAlaAlaGluGluGlnLysLeuProIleAsnAlaLeuSerAsnSerLeuLeuArgHis
3602  TGCGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCAC
      ACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTG
            ^            ^                                        ^
3606 SAC2, 3617 ALWN1, 3661 PFLM1,


      HisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThr
3662  CACAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGAAAGTCACA
      GTGTTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGT
                                    ^
3687 DRA3,


      PheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAla
```

FIG. 11-Page 6

pCMV–NS34A

```
5801  CAAGTCATTC TGAGAATAGT GTATGCGGCG ACCGAGTTGC TCTTGCCCGG
      GTTCAGTAAG ACTCTTATCA CATACGCCGC TGGCTCAACG AGAACGGGCC

5851  CGTCAATACG GGATAATACC GCGCCACATA GCAGAACTTT AAAAGTGCTC
      GCAGTTATGC CCTATTATGG CGCGGTGTAT CGTCTTGAAA TTTTCACGAG

5901  ATCATTGGAA AACGTTCTTC GGGGCGAAAA CTCTCAAGGA TCTTACCGCT
      TAGTAACCTT TTGCAAGAAG CCCCGCTTTT GAGAGTTCCT AGAATGGCGA

5951  GTTGAGATCC AGTTCGATGT AACCCACTCG TGCACCCAAC TGATCTTCAG
      CAACTCTAGG TCAAGCTACA TTGGGTGAGC ACGTGGGTTG ACTAGAAGTC

6001  CATCTTTTAC TTTCACCAGC GTTTCTGGGT GAGCAAAAAC AGGAAGGCAA
      GTAGAAAATG AAAGTGGTCG CAAAGACCCA CTCGTTTTTG TCCTTCCGTT

6051  AATGCCGCAA AAAAGGGAAT AAGGGCGACA CGGAAATGTT GAATACTCAT
      TTACGGCGTT TTTTCCCTTA TTCCCGCTGT GCCTTTACAA CTTATGAGTA

6101  ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA
      TGAGAAGGAA AAAGTTATAA TAACTTCGTA AATAGTCCCA ATAACAGAGT

6151  TGAGCGGATA CATATTTGAA TGTATTTAGA AAAATAAACA AATAGGGGTT
      ACTCGCCTAT GTATAAACTT ACATAAATCT TTTTATTTGT TTATCCCCAA

6201  CCGCGCACAT TTCCCCGAAA AGTGCCACCT GACGTCTAAG AAACCATTAT
      GGCGCGTGTA AAGGGGCTTT TCACGGTGGA CTGCAGATTC TTTGGTAATA

6251  TATCATGACA TTAACCTATA AAAATAGGCG TATCACGAGG CCCTTTCGTC
      ATAGTACTGT AATTGGATAT TTTTATCCGC ATAGTGCTCC GGGAAAGCAG
```

FIG. 9–Page 8

```
4851   AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTTCTTGA AGTGGTGGCC
       TCGTCTCGCT CCATACATCC GCCACGATGT CTCAAGAACT TCACCACCGG


4901   TAACTACGGC TACACTAGAA GGACAGTATT TGGTATCTGC GCTCTGCTGA
       ATTGATGCCG ATGTGATCTT CCTGTCATAA ACCATAGACG CGAGACGACT


4951   AGCCAGTTAC CTTCGGAAAA AGAGTTGGTA GCTCTTGATC CGGCAAACAA
       TCGGTCAATG GAAGCCTTTT TCTCAACCAT CGAGAACTAG GCCGTTTGTT


5001   ACCACCGCTG GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC AGATTACGCG
       TGGTGGCGAC CATCGCCACC AAAAAAACAA ACGTTCGTCG TCTAATGCGC


5051   CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT ACGGGGTCTG
       GTCTTTTTTT CCTAGAGTTC TTCTAGGAAA CTAGAAAAGA TGCCCCAGAC


5101   ACGCTCAGTG GAACGAAAAC TCACGTTAAG GGATTTTGGT CATGAGATTA
       TGCGAGTCAC CTTGCTTTTG AGTGCAATTC CCTAAAACCA GTACTCTAAT


5151   TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAAAAAT GAAGTTTTAA
       AGTTTTTCCT AGAAGTGGAT CTAGGAAAAT TTAATTTTTA CTTCAAAATT


5201   ATCAATCTAA AGTATATATG AGTAAACTTG GTCTGACAGT TACCAATGCT
       TAGTTAGATT TCATATATAC TCATTTGAAC CAGACTGTCA ATGGTTACGA


5251   TAATCAGTGA GGCACCTATC TCAGCGATCT GTCTATTTCG TTCATCCATA
       ATTAGTCACT CCGTGGATAG AGTCGCTAGA CAGATAAAGC AAGTAGGTAT


5301   GTTGCCTGAC TCCCCGTCGT GTAGATAACT ACGATACGGG AGGGCTTACC
       CAACGGACTG AGGGGCAGCA CATCTATTGA TGCTATGCCC TCCCGAATGG


5351   ATCTGGCCCC AGTGCTGCAA TGATACCGCG AGACCCACGC TCACCGGCTC
       TAGACCGGGG TCACGACGTT ACTATGGCGC TCTGGGTGCG AGTGGCCGAG


5401   CAGATTTATC AGCAATAAAC CAGCCAGCCG GAAGGGCCGA GCGCAGAAGT
       GTCTAAATAG TCGTTATTTG GTCGGTCGGC CTTCCCGGCT CGCGTCTTCA


5451   GGTCCTGCAA CTTTATCCGC CTCCATCCAG TCTATTAATT GTTGCCGGGA
       CCAGGACGTT GAAATAGGCG GAGGTAGGTC AGATAATTAA CAACGGCCCT


5501   AGCTAGAGTA AGTAGTTCGC CAGTTAATAG TTTGCGCAAC GTTGTTGCCA
       TCGATCTCAT TCATCAAGCG GTCAATTATC AAACGCGTTG CAACAACGGT


5551   TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT GGCTTCATTC
       AACGATGTCC GTAGCACCAC AGTGCGAGCA GCAAACCATA CCGAAGTAAG


5601   AGCTCCGGTT CCCAACGATC AAGGCGAGTT ACATGATCCC CCATGTTGTG
       TCGAGGCCAA GGGTTGCTAG TTCCGCTCAA TGTACTAGGG GGTACAACAC


5651   CAAAAAAGCG GTTAGCTCCT TCGGTCCTCC GATCGTTGTC AGAAGTAAGT
       GTTTTTTCGC CAATCGAGGA AGCCAGGAGG CTAGCAACAG TCTTCATTCA


5701   TGGCCGCAGT GTTATCACTC ATGGTTATGG CAGCACTGCA TAATTCTCTT
       ACCGGCGTCA CAATAGTGAG TACCAATACC GTCGTGACGT ATTAAGAGAA


5751   ACTGTCATGC CATCCGTAAG ATGCTTTTCT GTGACTGGTG AGTACTCAAC
       TGACAGTACG GTAGGCATTC TACGAAAAGA CACTGACCAC TCATGAGTTG
```

FIG. 9-Page 7

pCMV-NS34A

```
      +2 C  V  V  I  V  G  R  V  V  L  S  G  K  P  A  I  I
  3951 GCGTGGTCAT AGTGGGCAGG GTCGTCTTGT CCGGGAAGCC GGCAATCATA
       CGCACCAGTA TCACCCGTCC CAGCAGAACA GGCCCTTCGG CCGTTAGTAT
```

```
      +2 P  D  R  E  V  L  Y  R  E  F  D  E  M  E  E  C
  4001 CCTGACAGGG AAGTCCTCTA CCGAGAGTTC GATGAGATGG AAGAGTGCTA
       GGACTGTCCC TTCAGGAGAT GGCTCTCAAG CTACTCTACC TTCTCACGAT
```

```
       BamHI      MluI
       ~~~~~~     ~~~~~~
  4051 GGATCCACTA CGCGTTAGAG CTCGCTGATC AGCCTCGACT GTGCCTTCTA
       CCTAGGTGAT GCGCAATCTC GAGCGACTAG TCGGAGCTGA CACGGAAGAT
```

```
  4101 GTTGCCAGCC ATCTGTTGTT TGCCCCTCCC CCGTGCCTTC CTTGACCCTG
       CAACGGTCGG TAGACAACAA ACGGGGAGGG GGCACGGAAG GAACTGGGAC
```

```
  4151 GAAGGTGCCA CTCCCACTGT CCTTTCCTAA TAAAATGAGG AAATTGCATC
       CTTCCACGGT GAGGGTGACA GGAAAGGATT ATTTTACTCC TTTAACGTAG
```

```
  4201 GCATTGTCTG AGTAGGTGTC ATTCTATTCT GGGGGGTGGG GTGGGGCAGG
       CGTAACAGAC TCATCCACAG TAAGATAAGA CCCCCCACCC CACCCCGTCC
```

```
  4251 ACAGCAAGGG GGAGGATTGG GAAGACAATA GCAGGCATGC TGGGGAGCTC
       TGTCGTTCCC CCTCCTAACC CTTCTGTTAT CGTCCGTACG ACCCCTCGAG
```

```
  4301 TTCCGCTTCC TCGCTCACTG ACTCGCTGCG CTCGGTCGTT CGGCTGCGGC
       AAGGCGAAGG AGCGAGTGAC TGAGCGACGC GAGCCAGCAA GCCGACGCCG
```

```
  4351 GAGCGGTATC AGCTCACTCA AAGGCGGTAA TACGGTTATC CACAGAATCA
       CTCGCCATAG TCGAGTGAGT TTCCGCCATT ATGCCAATAG GTGTCTTAGT
```

```
  4401 GGGGATAACG CAGGAAAGAA CATGTGAGCA AAAGGCCAGC AAAAGGCCAG
       CCCCTATTGC GTCCTTTCTT GTACACTCGT TTTCCGGTCG TTTTCCGGTC
```

```
  4451 GAACCGTAAA AAGGCCGCGT TGCTGGCGTT TTTCCATAGG CTCCGCCCCC
       CTTGGCATTT TTCCGGCGCA ACGACCGCAA AAAGGTATCC GAGGCGGGGG
```

```
  4501 CTGACGAGCA TCACAAAAAT CGACGCTCAA GTCAGAGGTG GCGAAACCCG
       GACTGCTCGT AGTGTTTTTA GCTGCGAGTT CAGTCTCCAC CGCTTTGGGC
```

```
  4551 ACAGGACTAT AAAGATACCA GGCGTTTCCC CCTGGAAGCT CCCTCGTGCG
       TGTCCTGATA TTTCTATGGT CCGCAAAGGG GGACCTTCGA GGGAGCACGC
```

```
  4601 CTCTCCTGTT CCGACCCTGC CGCTTACCGG ATACCTGTCC GCCTTTCTCC
       GAGAGGACAA GGCTGGGACG GCGAATGGCC TATGGACAGG CGGAAAGAGG
```

```
  4651 CTTCGGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT
       GAAGCCCTTC GCACCGCGAA AGAGTTACGA GTGCGACATC CATAGAGTCA
```

```
  4701 TCGGTGTAGG TCGTTCGCTC CAAGCTGGGC TGTGTGCACG AACCCCCCGT
       AGCCACATCC AGCAAGCGAG GTTCGACCCG ACACACGTGC TTGGGGGGCA
```

```
  4751 TCAGCCCGAC CGCTGCGCCT TATCCGGTAA CTATCGTCTT GAGTCCAACC
       AGTCGGGCTG GCGACGCGGA ATAGGCCATT GATAGCAGAA CTCAGGTTGG
```

```
  4801 CGGTAAGACA CGACTTATCG CCACTGGCAG CAGCCACTGG TAACAGGATT
       GCCATTCTGT GCTGAATAGC GGTGACCGTC GTCGGTGACC ATTGTCCTAA
```

FIG. 9-Page 6

2486 ASE1, 2503 APAI,

```
          ProAlaProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIle
2522      CCTGCGCCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATA
          GGACGCGGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTAT
```

2559 PSTI,

```
          ArgGlnValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysPro
2582      AGGCAGGTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCG
          TCCGTCCACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGC
```

2600 DRA3,

```
          CysGlnValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPhe
2642      TGCCAGGTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTT
          ACGGTCCAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAA
```

```
          AlaProProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGlu
2702      GCGCCCCCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAA
          CGCGGGGGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTT
```

```
          TyrProValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSer
2762      TACCCGGTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCC
          ATGGGCCATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGG
```

2763 HGIE2, 2815 AAT2,

```
          MetLeuThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGly
2822      ATGCTCACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGA
          TACGAGTGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCT
```

2856 EAG1 XMA3,

```
          SerProProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAla
2882      TCACCCCCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCA
          AGTGGGGGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGT
```

2895 BALI, 2909 NHEI,

```
          ThrCysThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrp
2942      ACTTGCACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGG
          TGAACGTGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACC
```

2972 ESP1, 2975 SACI,

```
          ArgGlnGluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeu
3002      AGGCAGGAGATGGGCGGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTG
          TCCGTCCTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGAC
```

```
          AspSerPheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGlu
3062      GACTCCTTCGATCCGCTTGTGGCGGAGGAGGACGAGCGGGAGATCTCCGTACCCGCAGAA
          CTGAGGAAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTT
```

3102 BGL2,

FIG. 11-Page 5

```
      +2  G  D  F  D  S  V  I    D  C  N    T  C  V  T    Q  T  V
      3251 GGCGACTTCG ACTCGGTGAT AGACTGCAAT ACGTGTGTCA CCCAGACAGT
           CCGCTGAAGC TGAGCCACTA TCTGACGTTA TGCACACAGT GGGTCTGTCA
```

```
      +2     D  F  S  L  D  P  T    F  T  I    E  T  I    T  L  P
      3301 CGATTTCAGC CTTGACCCTA CCTTCACCAT TGAGACAATC ACGCTCCCCC
           GCTAAAGTCG GAACTGGGAT GGAAGTGGTA ACTCTGTTAG TGCGAGGGGG
```

```
      +2  Q  D  A  V    S  R  T    Q  R  R  G    R  T  G    R  G  K
      3351 AAGATGCTGT CTCCCGCACT CAACGTCGGG GCAGGACTGG CAGGGGGAAG
           TTCTACGACA GAGGGCGTGA GTTGCAGCCC CGTCCTGACC GTCCCCCTTC
```

```
      +2  P  G  I  Y    R  F  V    A  P  G    E  R  P  S    G  M  F
      3401 CCAGGCATCT ACAGATTTGT GGCACCGGGG GAGCGCCCCT CCGGCATGTT
           GGTCCGTAGA TGTCTAAACA CCGTGGCCCC CTCGCGGGGA GGCCGTACAA
```

```
      +2  D  S  S    V  L  C  E    C  Y  D    A  G  C    A  W  Y
      3451 CGACTCGTCC GTCCTCTGTG AGTGCTATGA CGCAGGCTGT GCTTGGTATG
           GCTGAGCAGG CAGGAGACAC TCACGATACT GCGTCCGACA CGAACCATAC
```

```
      +2  E  L  T  P    A  E  T    T  V  R  L    R  A  Y    M  N  T
      .3501 AGCTCACGCC CGCCGAGACT ACAGTTAGGC TACGAGCGTA CATGAACACC
            TCGAGTGCGG GCGGCTCTGA TGTCAATCCG ATGCTCGCAT GTACTTGTGG
```

```
      +2  P  G  L  P    V  C  Q    D  H  L    E  F  W  E    G  V  F
      3551 CCGGGGCTTC CCGTGTGCCA GGACCATCTT GAATTTTGGG AGGGCGTCTT
           GGCCCCGAAG GGCACACGGT CCTGGTAGAA CTTAAAACCC TCCCGCAGAA
```

```
      +2     T  G  L    T  H  I  D    A  H  F    L  S  Q    T  K  Q
              StuI
            ~~~~~~
      3601 TACAGGCCTC ACTCATATAG ATGCCCACTT TCTATCCCAG ACAAAGCAGA
           ATGTCCGGAG TGAGTATATC TACGGGTGAA AGATAGGGTC TGTTTCGTCT
```

```
      +2  S  G  E  N    L  P  Y    L  V  A  Y    Q  A  T    V  C  A
      3651 GTGGGGAGAA CCTTCCTTAC CTGGTAGCGT ACCAAGCCAC CGTGTGCGCT
           CACCCCTCTT GGAAGGAATG GACCATCGCA TGGTTCGGTG GCACACGCGA
```

```
      +2  R  A  Q  A    P  P  P    S  W  D    Q  M  W  K    C  L  I
      3701 AGGGCTCAAG CCCCTCCCCC ATCGTGGGAC CAGATGTGGA AGTGTTTGAT
           TCCCGAGTTC GGGGAGGGGG TAGCACCCTG GTCTACACCT TCACAAACTA
```

```
      +2  R  L  K    P  T  L  H    G  P  T    P  L  L    Y  R  L
      3751 TCGCCTCAAG CCCACCCTCC ATGGGCCAAC ACCCCTGCTA TACAGACTGG
           AGCGGAGTTC GGGTGGGAGG TACCCGGTTG TGGGGACGAT ATGTCTGACC
```

```
      +2 G  A  V  Q    N  E  I    T  L  T  H    P  V  T    K  Y  I
      3801 GCGCTGTTCA GAATGAAATC ACCCTGACGC ACCCAGTCAC CAAATACATC
           CGCGACAAGT CTTACTTTAG TGGGACTGCG TGGGTCAGTG GTTTATGTAG
```

```
      +2  M  T  C  M    S  A  D    L  E  V    V  T  S  T    W  V  L
      3851 ATGACATGCA TGTCGGCCGA CCTGGAGGTC GTCACGAGCA CCTGGGTGCT
           TACTGTACGT ACAGCCGGCT GGACCTCCAG CAGTGCTCGT GGACCCACGA
```

```
      +2  V  G  G    V  L  A  A    L  A  A    Y  C  L    S  T  G
      3901 CGTTGGCGGC GTCCTGGCTG CTTTGGCCGC GTATTGCCTG TCAACAGGCT
           GCAACCGCCG CAGGACCGAC GAAACCGGCG CATAACGGAC AGTTGTCCGA
```

FIG. 9-Page 5

```
      +2   N  S  S    P  P  V  V    P  Q  S    F  Q  V    A  H  L
2551   TAACTCCTCT CCACCAGTAG TGCCCCAGAG CTTCCAGGTG GCTCACCTCC
       ATTGAGGAGA GGTGGTCATC ACGGGGTCTC GAAGGTCCAC CGAGTGGAGG
```

```
      +2   H  A  P  T    G  S  G    K  S  T  K    V  P  A    A  Y  A
2601   ATGCTCCCAC AGGCAGCGGC AAAAGCACCA AGGTCCCGGC TGCATATGCA
       TACGAGGGTG TCCGTCGCCG TTTTCGTGGT TCCAGGGCCG ACGTATACGT
```

```
      +2   A  Q  G  Y    K  V  L    V  L  N    P  S  V    A  A  T  L
2651   GCTCAGGGCT ATAAGGTGCT AGTACTCAAC CCCTCTGTTG CTGCAACACT
       CGAGTCCCGA TATTCCACGA TCATGAGTTG GGGAGACAAC GACGTTGTGA
```

```
      +2   G  F  G    A  Y  M    S  K  A  H    G  I  D    P  N  I
2701   GGGCTTTGGT GCTTACATGT CCAAGGCTCA TGGGATCGAT CCTAACATCA
       CCCGAAACCA CGAATGTACA GGTTCCGAGT ACCCTAGCTA GGATTGTAGT
```

```
      +2   R  T  G  V    R  T  I    T  T  G  S    P  I  T    Y  S  T
2751   GGACCGGGGT GAGAACAATT ACCACTGGCA GCCCCATCAC GTACTCCACC
       CCTGGCCCCA CTCTTGTTAA TGGTGACCGT CGGGGTAGTG CATGAGGTGG
```

```
      +2   Y  G  K  F    L  A  D    G  G  C    S  G  G    A  Y  D  I
2801   TACGGCAAGT TCCTTGCCGA CGGCGGGTGC TCGGGGGGCG CTTATGACAT
       ATGCCGTTCA AGGAACGGCT GCCGCCCACG AGCCCCCCGC GAATACTGTA
```

```
      +2   I  I  C    D  E  C  H    S  T  D    A  T  S    I  L  G
2851   AATAATTTGT GACGAGTGCC ACTCCACGGA TGCCACATCC ATCTTGGGCA
       TTATTAAACA CTGCTCACGG TGAGGTGCCT ACGGTGTAGG TAGAACCCGT
```

```
      +2  I  G  T  V    L  D  Q    A  E  T  A    G  A  R    L  V  V
2901   TTGGCACTGT CCTTGACCAA GCAGAGACTG CGGGGGCGAG ACTGGTTGTG
       AACCGTGACA GGAACTGGTT CGTCTCTGAC GCCCCCGCTC TGACCAACAC
```

```
      +2   L  A  T  A    T  P  P    G  S  V    T  V  P  H    P  N  I
2951   CTCGCCACCG CCACCCCTCC GGGCTCCGTC ACTGTGCCCC ATCCCAACAT
       GAGCGGTGGC GGTGGGGAGG CCCGAGGCAG TGACACGGGG TAGGGTTGTA
```

```
      +2   E  E  V    A  L  S  T    T  G  E    I  P  F    Y  G  K
3001   CGAGGAGGTT GCTCTGTCCA CCACCGGAGA GATCCCTTTT TACGGCAAGG
       GCTCCTCCAA CGAGACAGGT GGTGGCCTCT CTAGGGAAAA ATGCCGTTCC
```

```
      +2   A  I  P  L    E  V  I    K  G  G  R    H  L  I    F  C  H
3051   CTATCCCCCT CGAAGTAATC AAGGGGGGGA GACATCTCAT CTTCTGTCAT
       GATAGGGGGA GCTTCATTAG TTCCCCCCCT CTGTAGAGTA GAAGACAGTA
```

```
      +2   S  K  K  K    C  D  E    L  A  A    K  L  V    A  L  G  I
3101   TCAAAGAAGA AGTGCGACGA ACTCGCCGCA AAGCTGGTCG CATTGGGCAT
       AGTTTCTTCT TCACGCTGCT TGAGCGGCGT TTCGACCAGC GTAACCCGTA
```

```
      +2   N  A  V    A  Y  Y  R    G  L  D    V  S  V    I  P  T
3151   CAATGCCGTG GCCTACTACC GCGGTCTTGA CGTGTCCGTC ATCCCGACCA
       GTTACGGCAC CGGATGATGG CGCCAGAACT GCACAGGCAG TAGGGCTGGT
```

```
      +2   S  G  D  V    V  V  V    A  T  D  A    L  M  T    G  Y  T
3201   GCGGCGATGT TGTCGTCGTG GCAACCGATG CCCTCATGAC CGGCTATACC
       CGCCGCTACA ACAGCAGCAC CGTTGGCTAC GGGAGTACTG GCCGATATGG
```

FIG. 9-Page 4

```
1851   TTAACGGTGG AGGGCAGTGT AGTCTGAGCA GTACTCGTTG CTGCCGCGCG
       AATTGCCACC TCCCGTCACA TCAGACTCGT CATGAGCAAC GACGGCGCGC


1901   CGCCACCAGA CATAATAGCT GACAGACTAA CAGACTGTTC CTTTCCATGG
       GCGGTGGTCT GTATTATCGA CTGTCTGATT GTCTGACAAG GAAAGGTACC


       +2                                                M  A  P
                                        EcoRI
                                        ~~~~~~
1951   GTCTTTTCTG CAGTCACCGT CGTCGACCTA AGAATTCACC ATGGCGCCCA
       CAGAAAAGAC GTCAGTGGCA GCAGCTGGAT TCTTAAGTGG TACCGCGGGT


       +2 I  T  A  Y   A  Q  Q   T  R  G   L   L  G  C   I  I  T
2001   TCACGGCGTA CGCCCAGCAG ACAAGGGGCC TCCTAGGGTG CATAATCACC
       AGTGCCGCAT GCGGGTCGTC TGTTCCCCGG AGGATCCCAC GTATTAGTGG


       +2 S  L  T  G   R  D  K   N  Q  V   E  G  E  V   Q  I  V
2051   AGCCTAACTG GCCGGGACAA AAACCAAGTG GAGGGTGAGG TCCAGATTGT
       TCGGATTGAC CGGCCCTGTT TTTGGTTCAC CTCCCACTCC AGGTCTAACA


       +2 S  T  A   A  Q  T  F   L  A  T   C  I  N   G  V  C
2101   GTCAACTGCT GCCCAAACCT TCCTGGCAAC GTGCATCAAT GGGGTGTGCT
       CAGTTGACGA CGGGTTTGGA AGGACCGTTG CACGTAGTTA CCCCACACGA


       +2 W  T  V  Y   H  G  A   G  T  R  T   I  A  S   P  K  G
2151   GGACTGTCTA CCACGGGGCC GGAACGAGGA CCATCGCGTC ACCCAAGGGT
       CCTGACAGAT GGTGCCCCGG CCTTGCTCCT GGTAGCGCAG TGGGTTCCCA


       -2 P  V  I  Q   M  Y  T   N  V  D   Q  D  L  V   G  W  P
2201   CCTGTCATCC AGATGTATAC CAATGTAGAC CAAGACCTTG TGGGCTGGCC
       GGACAGTAGG TCTACATATG GTTACATCTG GTTCTGGAAC ACCCGACCGG


       +2 A  S  Q   G  T  R  S   L  T  P   C  T  C   G  S  S
2251   CGCTTCGCAA GGTACCCGCT CATTGACACC CTGCACTTGC GGCTCCTCGG
       GCGAAGCGTT CCATGGGCGA GTAACTGTGG GACGTGAACG CCGAGGAGCC


       +2 D  L  Y  L   V  T  R   H  A  D  V   I  P  V   R  R  R
2301   ACCTTTACCT GGTCACGAGG CACGCCGATG TCATTCCCGT GCGCCGGCGG
       TGGAAATGGA CCAGTGCTCC GTGCGGCTAC AGTAAGGGCA CGCGGCCGCC


       +2 G  D  S  R   G  S  L   L  S  P   R  P  I  S   Y  L  K
2351   GGTGATAGCA GGGGCAGCCT GCTGTCGCCC CGGCCCATTT CCTACTTGAA
       CCACTATCGT CCCCGTCGGA CGACAGCGGG GCCGGGTAAA GGATGAACTT


       +2 G  S  S   G  G  P  L   L  C  P   A  G  H   A  V  G
2401   AGGCTCCTCG GGGGGTCCGC TGTTGTGCCC CGCGGGGCAC GCCGTGGGCA
       TCCGAGGAGC CCCCCAGGCG ACAACACGGG GCGCCCCGTG CGGCACCCGT


       +2 I  F  R  A   A  V  C   T  R  G  V   A  K  A   V  D  F
2451   TATTTAGGGC CGCGGTGTGC ACCCGTGGAG TGGCTAAGGC GGTGGACTTT
       ATAAATCCCG GCGCCACACG TGGGCACCTC ACCGATTCCG CCACCTGAAA


       +2 I  P  V  E   N  L  E   T  T  M   R  S  P  V   F  T  D
2501   ATCCCTGTGG AGAACCTAGA GACAACCATG AGGTCCCCGG TGTTCACGGA
       TAGGGACACC TCTTGGATCT CTGTTGGTAC TCCAGGGGCC ACAAGTGCCT
```

FIG. 9-Page 3

```
901   TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ATAACCCCGC
      AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TATTGGGGCG

951   CCCGTTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA
      GGGCAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT

1001  GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG CCATCCACGC
      CGTCTCGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC GGTAGGTGCG

1051  TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGCGGCCG
      ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCGCCGGC

1101  GGAACGGTGC ATTGGAACGC GGATTCCCCG TGCCAAGAGT GACGTAAGTA
      CCTTGCCACG TAACCTTGCG CCTAAGGGGC ACGGTTCTCA CTGCATTCAT

1151  CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA
      GGCGGATATC TGAGATATCC GTGTGGGGAA ACCGAGAATA CGTACGATAT

1201  CTGTTTTTGG CTTGGGGCCT ATACACCCCC GCTCCTTATG CTATAGGTGA
      GACAAAAACC GAACCCCGGA TATGTGGGGG CGAGGAATAC GATATCCACT

1251  TGGTATAGCT TAGCCTATAG GTGTGGGTTA TTGACCATTA TTGACCACTC
      ACCATATCGA ATCGGATATC CACACCCAAT AACTGGTAAT AACTGGTGAG

1301  CCCTATTGGT GACGATACTT TCCATTACTA ATCCATAACA TGGCTCTTTG
      GGGATAACCA CTGCTATGAA AGGTAATGAT TAGGTATTGT ACCGAGAAAC

1351  CCACAACTAT CTCTATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT
      GGTGTTGATA GAGATAACCG ATATACGGTT ATGAGACAGG AAGTCTCTGA

1401  GACACGGACT CTGTATTTTT ACAGGATGGG GTCCATTTAT TATTTACAAA
      CTGTGCCTGA GACATAAAAA TGTCCTACCC CAGGTAAATA ATAAATGTTT

1451  TTCACATATA CAACAACGCC GTCCCCCGTG CCCGCAGTTT TTATTAAACA
      AAGTGTATAT GTTGTTGCGG CAGGGGGCAC GGGCGTCAAA AATAATTTGT

1501  TAGCGTGGGA TCTCCGACAT CTCGGGTACG TGTTCCGGAC ATGGGCTCTT
      ATCGCACCCT AGAGGCTGTA GAGCCCATGC ACAAGGCCTG TACCCGAGAA

1551  CTCCGGTAGC GGCGGAGCTT CCACATCCGA GCCCTGGTCC CATCCGTCCA
      GAGGCCATCG CCGCCTCGAA GGTGTAGGCT CGGGACCAGG GTAGGCAGGT

1601  GCGGCTCATG GTCGCTCGGC AGCTCCTTGC TCCTAACAGT GGAGGCCAGA
      CGCCGAGTAC CAGCGAGCCG TCGAGGAACG AGGATTGTCA CCTCCGGTCT

1651  CTTAGGCACA GCACAATGCC CACCACCACC AGTGTGCCGC ACAAGGCCGT
      GAATCCGTGT CGTGTTACGG GTGGTGGTGG TCACACGGCG TGTTCCGGCA

1701  GGCGGTAGGG TATGTGTCTG AAAATGAGCT CGGAGATTGG GCTCGCACCT
      CCGCCATCCC ATACACAGAC TTTTACTCGA GCCTCTAACC CGAGCGTGGA

1751  GGACGCAGAT GGAAGACTTA AGGCAGCGGC AGAAGAAGAT GCAGGCAGCT
      CCTGCGTCTA CCTTCTGAAT TCCGTCGCCG TCTTCTTCTA CGTCCGTCGA

1801  GAGTTGTTGT ATTCTGATAA GAGTCAGAGG TAACTCCCGT TGCGGTGCTG
      CTCAACAACA TAAGACTATT CTCAGTCTCC ATTGAGGGCA ACGCCACGAC
```

FIG. 9-Page 2

pCMV-NS34A

```
  1   TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG
      AGCGCGCAAA GCCACTACTG CCACTTTTGG AGACTGTGTA CGTCGAGGGC

 51   GAGACGGTCA CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG
      CTCTGCCAGT GTCGAACAGA CATTCGCCTA CGGCCCTCGT CTGTTCGGGC

101   TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG
      AGTCCCGCGC AGTCGCCCAC AACCGCCCAC AGCCCCGACC GAATTGATAC

151   CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGAA GCTTTTTGCA
      GCCGTAGTCT CGTCTAACAT GACTCTCACG TGGTATACTT CGAAAAACGT
```

                  StuI
                  ~~~~~~~
```
201   AAAGCCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG
      TTTCGGATCC GGAGGTTTTT TCGGAGGAGT GATGAAGACC TTATCGAGTC

251   AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA
      TCCGGCTCCG CCGGAGCCGG AGACGTATTT ATTTTTTTTA ATCAGTCGGT

301   TGGGGCGGAG AATGGGCGGA ACTGGGCGGG GAGGGAATTA TTGGCTATTG
      ACCCCGCCTC TTACCCGCCT TGACCCGCCC CTCCCTTAAT AACCGATAAC

351   GCCATTGCAT ACGTTGTATC TATATCATAA TATGTACATT TATATTGGCT
      CGGTAACGTA TGCAACATAG ATATAGTATT ATACATGTAA ATATAACCGA

401   CATGTCCAAT ATGACCGCCA TGTTGACATT GATTATTGAC TAGTTATTAA
      GTACAGGTTA TACTGGCGGT ACAACTGTAA CTAATAACTG ATCAATAATT

451   TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA TGGAGTTCCG
      ATCATTAGTT AATGCCCCAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC

501   CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC
      GCAATGTATT GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG

551   CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA
      GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT

601   GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT AAACTGCCCA
      CCCTGAAAGG TAACTGCAGT TACCCACCTC ATAAATGCCA TTTGACGGGT

651   CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTCCGCCC CCTATTGACG
      GAACCGTCAT GTAGTTCACA TAGTATACGG TTCAGGCGGG GGATAACTGC

701   TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA
      AGTTACTGCC ATTTACCGGG CGGACCGTAA TACGGGTCAT GTACTGGAAT

751   CGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC
      GCCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG

801   CATGGTGATG CGGTTTTGGC AGTACACCAA TGGGCGTGGA TAGCGGTTTG
      GTACCACTAC GCCAAAACCG TCATGTGGTT ACCCGCACCT ATCGCCAAAC

851   ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG
      TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT ACCCTCAAAC
```
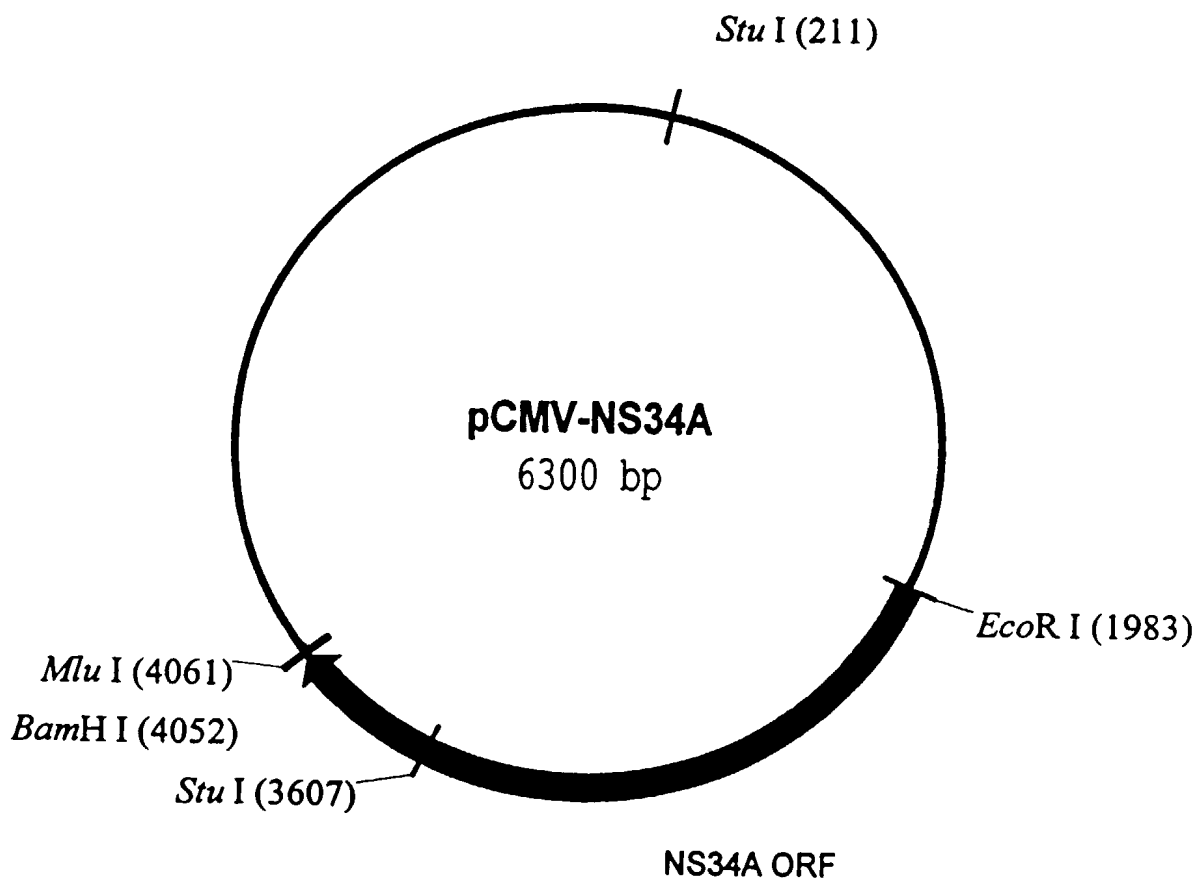
FIG. 9-Page 1

Stu I (211)

pCMV-NS34A
6300 bp

*Eco*R I (1983)

Mlu I (4061)

*Bam*H I (4052)

Stu I (3607)

NS34A ORF

FIG. 8

pCMV-II

3521 TTGCCATTGC TACAGGCATC GTGGTGTCAC GCTCGTCGTT TGGTATGGCT TCATTCAGCT CCGGTTCCCA ACGATCAAGG
     AACGGTAACG ATGTCCGTAG CACCACAGTG CGAGCAGCAA AGCATACCGA AGTAAGTCGA GGCCAAGGGT TGCTAGTTCC

3601 CGAGTTACAT GATCCCCCAT GTTGTGCAAA AAAGCGGTTA GCTCCTTCGG TCCTCCGATC GTTGTCAGAA GTAAGTTGGC
     GCTCAATGTA CTAGGGGGTA CAACACGTTT TTTCGCCAAT CGAGGAAGCC AGGAGGCTAG CAACAGTCTT CATTCAACCG

3681 CGCAGTGTTA TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA
     GCGTCACAAT AGTGAGTACC AATACCGTCG TGACGTATTA AGAGAATGAC AGTACGGTAG GCATTCTACG AAAAGACACT

3761 CTGGTGAGTA CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC AATACGGGAT
     GACCACTCAT GAGTTGGTTC AGTAAGACTC TTATCACATA CGCCGCTGGC TCAACGAGAA CGGGCCGCAG TTATGCCCTA

3841 AATACCCGCC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGGAAAACG TTCTTCGGGG CGAAAACTCT CAAGGATCTT
     TTATGGGCGG GTGTATCGTC TTGAAATTTT CACGAGTAGT AACCTTTTGC AAGAAGCCCC GCTTTTGAGA GTTCCTAGAA

3921 ACCGCTGTTG AGATCCAGTT CGATGTAACC CCACTCGTGCA CCCAACTGAT CTTCAGCATC TTTTACTTTC ACCAGCGTTT
     TGGCGACAAC TCTAGGTCAA GCTACATTGG GGTGAGCACGT GGGTTGACTA GAAGTCGTAG AAAATGAAAG TGGTCGCAAA

4001 CTGGGTGAGC AAAAACAGGA AGGCAAAATG CCGCAAAAAA GGGAATAAGG GCGACACGGA AATGTTGAAT ACTCATACTC
     GACCCACTCG TTTTTGTCCT TCCGTTTTAC GGCGTTTTTT CCCTTATTCC CGCTGTGCCT TTACAACTTA TGAGTATGAG

4081 TTCCTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA
     AAGGAAAAAG TTATAATAAC TTCGTAAATA GTCCCAATAA CAGAGTACTC GCCTATGTAT AAACTTACAT AAATCTTTTT

4161 TAAACAAATA GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA
     ATTTGTTTAT CCCCAAGGCG CGTGTAAAGG GGCTTTTCAC GGTGGACTGC AGATTCTTTG GTAATAATAG TACTGTAATT

4241 CCTATAAAAA TAGGCGTATC ACGAGGCCCT TTCGTC
     GGATATTTTT ATCCGCATAG TGCTCCGGGA AAGCAG

FIG. 7-Page 6

pCMV-II

2801   TGGCAGCAGC CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG GTGGCCTAAC
          ACCGTCGTCG GTGACCATTG TCCTAATCGT CTCGCTCCAT ACATCCGCCA CGATGTCTCA AGAACTTCAC CACCGGATTG

2881   TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC
          ATGCCGATGT GATCTTCCTG TCATAAACCA TAGACGCGAG ACGACTTCGG TCAATGGAAG CCTTTTTCTC AACCATCGAG

2961   TTGATCCGGC AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA AAAAAAGGAT
          AACTAGGCCG TTTGTTTGGT GGCGACCATC GCCACCAAAA AAACAAACGT TCGTCGTCTA ATGCGCGTCT TTTTTTCCTA

3041   CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCATG
          GAGTTCTTCT AGGAAACTAG AAAAGATGCC CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA AAACCAGTAC

3121   AGATTATCAA AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA
          TCTAATAGTT TTTCCTAGAA GTGGATCTAG GAAAATTTAA TTTTTACTTC AAAATTTAGT TAGATTTCAT ATATACTCAT

3201   AACTTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCGTTCA TCCATAGTTG
          TTGAACCAGA CTGTCAATGG TTACGAATTA GTCACTCCGT GGATAGAGTC GCTAGACAGA TAAAGCAAGT AGGTATCAAC

3281   CCTGACTCCC CGTCGTGTAG ATAACTACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT ACCGCGAGAC
          GGACTGAGGG GCAGCACATC TATTGATGCT ATGCCCCTCCC GAATGGTAGA CCGGGGTCAC GACGTTACTA TGGCGCTCTG

3361   CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT
          GGTGCGAGTG GCCGAGGTCT AAATAGTCGT TATTTGGTCG GTCGGCCTTC CCGGCTCGCG TCTTCACCAG GACGTTGAAA

3441   ATCCGCCTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG
          TAGGCGGAGG TAGGTCAGAT AATTAACAAC GGCCCTTCGA TCTCATTCAT CAAGCGGTCA ATTATCAAAC GCGTTGCAAC

FIG. 7-Page 5

pCMV-II

2081 CCAGCCATCT GTTGTTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAG GTGCCACTCC CACTGTCCTT TCCTAATAAA
     GGTCGGGTAGA CAACAAACGG GGAGGGGGCA CGGAAGGAAC TGGGACCTTC CACGGTGAGG GTGACAGGAA AGGATTATTT

2161 ATGAGGAAAT TGCATCGCAT TGTCTGAGTA GGTGTCATTC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG
     TACTCCTTTA ACGTAGCGTA ACAGACTCAT CCACAGTAAG ATAAGACCCC CCACCCCACC CCGTCCTGTC GTTCCCCCTC

2241 GATTGGGAAG ACAATAGCAG GCATGCTGGG GAGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG GTCGTTCGGC
     CTAACCCTTC TGTTATCGTC CGTACGACCC CTCGAGAAGG CGAAGGAGCG AGTGACTGAG CGACGCGAGC CAGCAAGCCG

2321 TGCGGCGAGC GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG
     ACGCCGCTCG CCATAGTCGA GTGAGTTTCC GCCATTATGC CAATAGGTGT CTTAGTCCCC TATTGCGTCC TTTCTTGTAC

2401 TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC GCCCCCCTGA
     ACTCGTTTTC CGGTCGTTTT CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG GTATCCGAGG CGGGGGGACT

2481 CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG
     GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT CTCCACCGCT TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC

2561 GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC GGGAAGCGTG
     CTTCGAGGGA GCACGCGAGA GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGGCGGA AAGAGGGAAG CCCTTCGCAC

2641 GCGCTTTCTC AATGCTCACG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
     CGCGAAAGAG TTACGAGTGC GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC ACGTGCTTGG

2721 CCCCGTTCAG CCCGACCGCT GGCGCCTTATC CGGTAACTAT CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC
     GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA GCAGAACTCA GGTTGGGCCA TTCTGTGCTG AATAGCGGTG

FIG. 7-Page 4

pCMV-II

```
1441   TATTTACAAA  TTCACATATA  CAACAACGCC  GTCCCCCGTG  CCCGCAGTTT  TTATTAAACA  TAGCGTGGGA  TCTCCGACAT
       ATAAATGTTT  AAGTGTATAT  GTTGTTGCGG  CAGGGGGCAC  GGGCGTCAAA  AATAATTTGT  ATCGCACCCT  AGAGGCTGTA

1521   CTCGGGTACG  TGTTCCGGAC  ATGGGCTCTT  CTCCGGTAGC  GGCGGGAGCTT  CCACATCCGA  GCCCTGGTCC  CATCCGTCCA
       GAGCCCATGC  ACAAGGCCTG  TACCCGAGAA  GAGGCCATCG  CCGCCCTCGAA  GGTGTAGGCT  CGGGACCAGG  GTAGGCAGGT

1601   GCGGCTCATG  GTCGGCTCGGC  AGCTCCTTGC  TCCTAACAGT  GGAGGCCAGA  CTTAGGCACA  GCACAATGCC  CACCACCACC
       CGCCGAGTAC  CAGCGAGCCG  TCGAGGAACG  AGGATTGTCA  CCTCCGGTCT  GAATCCGTGT  CGTGTTACGG  GTGGTGGTGG

1681   AGTGTGCCGC  ACAAGGCCGT  GGCGGTAGGG  TATGTGTCTG  AAAATGAGCT  CGGAGATTGG  GCTCGCACCT  GGACGCAGAT
       TCACACGGCG  TGTTCCGGCA  CCGCCATCCC  ATACACAGAC  TTTTACTCGA  GCCTCTAACC  CGAGCGTGGA  CCTGCGTCTA

1761   GGAAGACTTA  AGGCAGCGGC  AGAAGAAGAT  GCAGGCAGCT  GAGTTGTTGT  ATTCTGATAA  GAGTCAAGGG  TAACTCCCGT
       CCTTCTGAAT  TCCGTCGCCG  TCTTCTTCTA  CGTCCGTCGA  CTCAACAACA  TAAGACTATT  CTCAGTTCCC  ATTGAGGGCA

1841   TGCGGGTGCTG  TTAACGGGTGG  AGGGCAGTGT  AGTCTGAGCA  GTACTCGTTG  CTGCCCGGCGG  CGCCACCAGA  CATAATAGCT
       ACGCCACGAC  AATTGCCACC  TCCCGTCACA  TCAGACTCGT  CATGAGCAAC  GACGGGCGC   GCGGTGGTCT  GTATTATCGA

                                                                                    EcoRI
                                                                                    ------
1921   GACAGACTAA  CAGACTGTTC  CTTTCCATGG  GTCTTTTCTG  CAGTCACCGT  CGTCGACCTA  AGAATTCAGA  CTCGAGCAAG
       CTGTCTGATT  GTCTGACAAG  GAAAGGTACC  CAGAAAAGAC  GTCAGTGGCA  GCAGCTGGAT  TCTTAAGTCT  GAGCTCGTTC

        XbaI                    BamHI       MluI
        -----                   ------      ------
2001   TCTAGAAAGG  CGGCCCAAGA  TATCAAGGAT  CCACTACGCG  TTAGAGCTCG  CTGATCAGCC  TCGACTCTGC  CTTCTAGTTG
       AGATCTTTCC  GCCGGGTTCT  ATAGTTCCTA  GGTGATGCGC  AATCTCGAGC  GACTAGTCGG  AGCTGACACG  GAAGATCAAC
```

FIG. 7-Page 3

pCMV-II

```
721   GCCTGGCATT ATGCCCAGTA CATGACCTTA CGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC
      CGGACCGTAA TACGGGTCAT GTACTGGAAT GCCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG

801   CATGGTGATG CGGTTTTGGC AGTACACCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA
      GTACCACTAC GCCAAAACCG TCATGTGGTT ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT

881   TTGACGTCAA TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ATAACCCCGC CCCGTTGACG
      AACTGCAGTT ACCCTCAAAC AAAACCGTGG CCTGAAAGGT TTTACAGCAT TATTGGGGCG GGGCAACTGC

961   CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG
      GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC

1041  CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGCGGCCG GGAACGGGTG ATTGGAACGC
      GGTAGGTGCG ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCGCCGGC CCTTGCCCAC TAACCTTGCG

1121  GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA
      CCTAAGGGGC ACGGTTCTCA CTGCATTCAT GGCGGATATC TGAGATATCC GTGTGGGGAA ACCGAGAATA CGTACGATAT

1201  CTGTTTTTGG CTTGGGGCCT ATACACCCCC GCTCCTTATG CTATAGGTGA TGGTATAGCT TAGCCTATAG GTGTGGGTTA
      GACAAAAACC GAACCCCGGA TATGTGGGGG CGAGGAATAC GATATCCACT ACCATATCGA ATCGGGATAT CACACCCAAT

1281  TTGACCATTA TTGACCACTC CCCTATTGGT GACGATACTT TCCATTACTA ATCCATAACA TGGCTCTTTG CCACAACTAT
      AACTGGTAAT AACTGGTGAG GGGATAACCA CTGCTATGAA AGGTAATGAT TAGGTATTGT ACCGAGAAAC GGTGTTGATA

1361  CTCTATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT GACACGGACT CTGTATTTTT ACAGGATGGG GTCCATTTAT
      GAGATAACCG ATATACGGTT ATGAGACAGG AAGTCTCTGA CTGTGCCTGA GACATAAAAA TGTCCTACCC CAGGTAAATA
```

FIG. 7-Page 2

pCMV-II

```
   1  TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT
      AGCGGCCAAA GCCACTACTG CCACTTTTGG AGACTGTGTA CGTCGAGGGC CTCTGCCAGT GTCGAACAGA CATTCGCCTA

  81  GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA
      CGGCCCTCGT CTGTTCGGGC AGTCCCGCGC AGTCGCCCAC AACCGCCCAC AGCCCCGACC GAATTGATAC GCCGTAGTCT

 161  GCAGATTGTA CTGAGAGTGC ACCATATGAA GCTTTTTGCA AAAGCCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG
      CGTCTAACAT GACTCTCACG TGGTATACTT CGAAAAACGT TTTCGGATCC GGAGGTTTTT TCGGAGGAGT GATGAAGACC

 241  AATAGCTCAG AGGCCCGAGGC GGCCTCGCCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGGGGCGGAG AATGGGCGGA
      TTATCGAGTC TCCGGCTCCG CCGGAGCCGG AGACGTATTT ATTTTTTTTA ATCAGTCGGT ACCCCGCCTC TTACCCGCCT

 321  ACTGGGCGGG GAGGGAATTA TTGGCTATTG GCCATTGCAT ACGTTGTATC TATATCATAA TATGTACATT TATATTGGCT
      TGACCCGCCC CTCCCTTAAT AACCGATAAC CGGTAACGTA TGCAACATAG ATATAGTATT ATACATGTAA ATATAACCGA

 401  CATGTCCAAT ATGACCGCCA TGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT
      GTACAGGTTA TACTGGCGGT ACAACTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA

 481  AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCATT
      TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGCGGGTAA

 561  GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT
      CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTC ATAAATGCCA

 641  AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTCCGCCC CCTATTGACG TCAATGACGG TAAATGGCCC
      TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCAGGCGGG GGATAACTGC AGTTACTGCC ATTTACCGGG
```

FIG. 7-Page 1

pCMV-delNS35

```
8241   AGGACAGTAT TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA
       TCCTGTCATA AACCATAGAC GCGAGACGAC TTCGGTCAAT GGAAGCCTTT TTCTCAACCA TCGAGAACTA GGCCGTTTGT

8321   AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT
       TTGGTGGCGA CCATCGCCAC CAAAAAAACA AACGTTCGTC GTCTAATGCG CGTCTTTTTT TCCTAGAGTT CTTCTAGGAA

8401   TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACCTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG
       ACTAGAAAAG ATGCCCCAGA CTGCGAGTCA CCTTGCTTTT GAGTGGAATT CCCTAAAACC AGTACTCTAA TAGTTTTTCC

8481   ATCTTCACCT AGATCCTTTT AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG
       TAGAAGTGGA TCTAGGAAAA TTTAATTTTT ACTTCAAAAT TTAGTTAGAT TTCATATATA CTCATTTGAA CCAGACTGTC

8561   TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC GTTCATCCAT AGTTGCCTGA CTCCCCGTCG
       AATGGTTACG AATTAGTCAC TCCGTGGATA GAGTCGCTAG ACAGATAAAG CAAGTAGGTA TCAACGGACT GAGGGGCAGC

8641   TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT
       ACATCTATTG ATGCTATGCC CTCCCGAATG GTAGACCGGG GTCACGACGT TACTATGGCG CTCTGGGTGC GAGTGGCCGA

8721   CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA
       GGTCTAAATA GTCGTTATTT GGTCGGTCGG CCTTCCCGGC TCGCGTCTTC ACCAGGACGT TGAAATAGGC GGAGGTAGGT

8801   GTCTATTAAT TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA CGTTGTTGCC ATTGCTACAG
       CAGATAATTA ACAACGGCCC TTCGATCTCA TTCATCAAGC GGTCAATTAT CAAACGCGTT GCAACAACGG TAACGATGTC

8881   GCATCGTGGT GTCACGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC
       CGTAGCACCA CAGTGCGAGC AGCAAACCAT ACCGAAGTAA AGTCGAGGCCA GTTCCGCTCA ATGTACTAGG
```

FIG. 5-Page 15

```
7521   CGCATTGTCT GAGTAGGTGT CATTCTATTC TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGAAGACAAT
       GCGTAACAGA CTCATCCACA GTAAGATAAG ACCCCCCACC CCACCCCGTC CTGTCGTTCC CCTTCTGTTA

7601   AGCAGGCATG CTGGGGAGCT CTTCCGCTTC CTCGGCTCACT GACTCGGTCGT TCGGCTGCGCG CGAGCGGTAT
       TCGTCCGTAC GACCCCTCGA GAAGGCGAAG GAGCGAGTGA CTGAGCCAGCA AGCCGACGCG GCTCGCCATA

7681   CAGCTCACTC AAAGGCGGTA ATACGGTTAT CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG
       GTCGAGTGAG TTTCCGCCAT TATGCCAATA GGTGTCTTAG TCCCCTATTG CGTCCTTTCT TGTACACTCG TTTTCCGGTC

7761   CAAAAGGCCA GGAACCCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA
       GTTTTCCGGT CCTTGGGCATT TTTCCGGCGC AACGACCGCA AAAAGGTATC CGAGGCGGGG GGACTGCTCG TAGTGTTTTT

7841   TCGACGCTCA AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC
       AGCTGCGAGT TCAGTCTCCA CCGCTTTGGG CTGTCCTGAT ATTTCTATGG TCCGCAAAGG GGGACCTTCG AGGGAGCACG

7921   GCTCTCCTGT TCCGACCCCTG CGCCTTACCG GATACCCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC
       CGAGAGGACA AGGCTGGGGAC GGCGAATGGC CTATGGACAG GCGGAAAGAG GGAAGCCCTT CGCACCGCGA AAGAGTTACG

8001   TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA
       AGTGCGACAT CCATAGAGTC AAGCCACATC CAGCAAGCGA GGTTCGACCC GACACACGTG CTTGGGGGGC AAGTCGGGCT

8081   CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG
       GGCGACGCGG AATAGGCCAT TGATAGCAGA ACTCAGGTTG GCCATTCTG TGCTGAATAG CGGTGACCGT CGTCGGTGAC

8161   GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC CTAACTACGG CTACACTAGA
       CATTGTCCTA ATCGTCTCGC TCCATACATC CGCCACGATG TCTCAAGAAC TTCACCACCG GATTGATGCC GATGTGATCT
```

FIG. 5-Page 14

pCMV-delNS35

```
     +2   S   P   G   E   I   N   R   V   A   A   C   L   R   K   L   G   V   P   P   L   R   A   W   R   H   R
    6961  CTCTCCAGGT GAAATCAATA GGGTGGCCGC ATGCCTCAGA AAACTTGGGG TACCGCCCTT GCGAGCTTGG AGACACCGGG
          GAGAGGTCCA CTTTAGTTAT CCCACCGGCG TACGGAGTCT TTTGAACCCC ATGGCGGGAA CGCTCGAACC TCTGTGGCCC

     +2   A   R   S   V   R   A   R   L   L   A   R   G   G   R   A   A   I   C   G   K   Y   L   F   N   W   A   V
    7041  CCCGGAGCGT CCGCGCTAGG CTTCTGGCCA GAGGAGGCAG GGCTGCCATA TGTGGCAAGT ACCTCTTCAA CTGGGCAGTA
          GGGCCTCGCA GGCGCGATCC GAAGACCGGT CTCCTCCGTC CCGACGGTAT ACACCGTTCA TGGAGAAGTT GACCCGTCAT

     +2   R   T   K   L   K   L   T   P   I   A   A   A   G   Q   L   D   L   S   G   W   F   T   A   G   Y   S   G
    7121  AGAACAAAGC TCAAACTCAC TCCAATAGCG GCCCTGGCCC AGCTGGACTT GTCCGGGCTGG TTCACGGCTG GCTACAGCGG
          TCTTGTTTCG AGTTTGAGTG AGGTTATCGC CGGGACCGGG TCGACCTGAA CAGGCCCGACC AAGTGCCGAC CGATGTCGCC

     +2   G   D   I   Y   H   S   V   S   H   A   R   P   R   W   I   W   F   C   L   L   L   L   A   G   V
    7201  GGGAGACATT TATCACAGCG TGTCTCATGC CCGGCCCCGC TGGATCTGGT TTTGCCTACT CCTGCTTGCT GCAGGGGTAG
          CCCTCTGTAA ATAGTGTCGC ACAGAGTACG GGCCGGGGCG ACCTAGACCA AAACGGATGA GGACGAACGA CGTCCCCATC

     +2   G   I   Y   L   L   P   N   R
    7281  GCATCTACCT CCTCCCCAAC CGATGAAGGT TGGGGTAAAC ACTCCGGCCT AAAAAAAAAA AAAAAATCTAG AAAGGCCGC
          CGTAGATGGA GGAGGGGTTG GCTACTTCCA ACCCCATTTG TGAGGCCGGA TTTTTTTTTT TTTTTAGATC TTTCCCGGCG

                                         BamHI        MluI
                                         -----        -----
    7361  CAAGATATCA AGGATCCACT ACGCGTTAGA GCTCGCTGAT CAGCCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT
          GTTCTATAGT TCCTAGGTGA TGCGCAATCT CGAGCGACTA GTCGGGAGCTG ACACGGAAGA TCAACGGTCG GTAGACAACA

    7441  TTGCCCCTCC CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAATGAG GAAATTGCAT
          AACGGGGAGG GGGCACGGAA GGAACTGGGA CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC CTTTAACGTA
```

FIG. 5-Page 13

pCMV-delNS35

```
      N  T  L  T  C  Y  I  K  A  R    A  A  C  R  A  A  G    L  Q  D    C  T  M  L  V  C  G
+2
6401  AACACCCTCA CTTGCTACAT CAAGGCCCGG GCAGCCTGTC GAGCCGCCAGG GCTCCAGGAC TGCACCATGC TCGTGTGTGG
      TTGTGGGAGT GAACGATGTA GTTCCGGGCC CGTCGGACAG CTCGGCGGTCC CGAGTCCTG ACGTGGTACG AGCACACACC

      D  D  L  V  V  I  C  E  S  A    G  V  Q    E  D  A  A    S  L  R    A  F  T    E  A  M
+2
6481  CGACGACTTA GTCGTTATCT GTGAAAGCGC GGGGGTCCAG GAGGACGCGG CGAGCCTGAG AGCCTTCACG GAGGCTATGA
      GCTGCTGAAT CAGCAATAGA CACTTTCGCG CCCCCAGGTC CTCCTGCGCC GCTCGGACTC TCGGAAGTGC CTCCGATACT

      T  R  Y  S    A  P  P    G  D  P  P  Q  P  E    Y  D  L    E  L  I  T    S  C  S    S  N  V
+2
6561  CCAGTACTC CGCCCCCCCT GGGGACCCCC CACAACCAGA ATACGACTTG GAGCTCATAA CATCATGCTC CTCCAACGTG
      GGTCATGAG GCGGGGGGGA CCCCTGGGGG GTGTTGGTCT TATGCTGAAC CTCGAGTATT GTAGTACGAG GAGGTTGCAC

      S  V  A  H    D  G  A    G  K  R    V  Y  Y  L    T  R  D    P  T  T    P  L  A  R    A  A  W
+2
6641  TCAGTCGCCC ACGACGGCGC TGGAAAGAGG GTCTACTACC TCACCCGTGA CCCTACAACC GGGATGTTGG GAGCTGCCTG
      AGTCAGCGGG TGCTGCCGCG ACCTTTCTCC CAGATGATGG AGTGGGCACT GGGATGTTGG CTCGACGCAC

      E  T  A    R  H  T  P  V  N  S    W  L  G    N  I  I  M  F  A  P    T  L  W    A  R  M
+2
6721  GGAGACAGCA AGACACACTC CAGTCAATTC CTGGCTAGGC AACATAATCA TGTTTGCCCC CACACTGTGG GCGAGGATGA
      CCTCTGTCGT TCTGTGTGAG GTCAGTTAAG GACCGATCCG TTGTATTAGT ACAAACGGGG GTGTGACACC CGCTCCTACT

      I  L  M  T    H  F  F    S  V  L  I    A  R  D    Q  L  E    Q  A  L  D    C  E  I    Y  G  A
+2
6801  TACTGATGAC CCATTCTTT AGCGTCCTTA TAGCCAGGGA CCAGCTTGAA CAGGCCCTCG ATTGCGAGAT CTACGGGGCC
      ATGACTACTG GGTAAAGAAA TCGCAGGAAT ATCGGTCCCT GGTCGAACTT GTCCGGGAGC TAACGCTCTA GATGCCCCGG

      C  Y  S  I  E  P  L    D  L  P    P  I  I  Q  R  L  H    G  L  S    A  F  S  L  H  S  Y
+2
6881  TGCTACTCCA TAGAACCACT GGATCTACCT CCAATCATTC AAAGACTCCA TGGCCTCAGC GCATTTTCAC TCCACAGTTA
      ACGATGAGGT ATCTTGGTGA CCTAGATGGA GGTTAGTAAG TTTCTGAGGT ACCGGAGTCG CGTAAAAGTG AGGTGTCAAT
```

FIG. 5–Page 12

```
+2    Y  A  A  Q    G  Y  K    V  L  V  L    N  P  S    V  A  A    T  L  G  F    G  A  Y    M  S  K
2001  ATGCCAGCTCA GGGCTATAAG GTGCTAGTAC TCAACCCCTC TGTTGCTGCA ACACTGGGCT TTGGTGCTTA CATGTCCAAG
      TACGGTCGAGT CCCGATATTC CACGATCATG AGTTGGGGAG ACAACGACGT TGTGACCCGA AACCACGAAT GTACAGGTTC


+2    A  H  G  I    D  P  N    I  R  T    G  V  R  T    I  T  T    G  S  P    I  T  Y  S    T  Y  G
2081  GCTCATGGGA TCGATCCTAA CATCAGGACC GGGGTGAGAA CAATTACCAC TGGCAGCCCC ATCACGTACT CCACCTACGG
      CGAGTACCCT AGCTAGGATT GTAGTCCTGG CCCCACTCTT GTTAATGGTG ACCGTCGGGG TAGTGCATGA GGTGGATGCC


+2    K  F  L    A  D  G  G    C  S  G    G  A  Y    D  I  I  I    C  D  E    C  H  S    T  D  A
2161  CAAGTTCCTT GCCGACGGGCG GGTGCTCGGG GGGGCCTTAT GACATAATAA TTTGTGACGA GTGCCACTCC ACGGATGCCA
      GTTCAAGGAA CGGCTGCCGC CCACGAGCCC CCCCGGAATA CTGTATTATT AAACACTGCT CACGGTGAGG TGCCTACGGT


+2    T  S  I  L    G  I  G    T  V  L  D    Q  A  E    T  A  G    A  R  L    V  L  A    T  A  T
2241  CATCCATCTT GGGCATTGGC ACTGTCCTTG ACCAAGCAGA GACTGCGGGG GCGAGACTGG TTGTGCTCGC CACCGCCACC
      GTAGGTAGAA CCCGTAACCG TGACAGGAAC TGGTTCGTCT CTGACGCCCC CGCTCTGACC AACACGAGCG GTGGCGGTGG


+2    P  P  G  S    V  T  V    P  H  P    N  I  E  E    V  A  L    S  T  T    G  E  I  P    F  Y  G
2321  CCTCCGGGGCT CCGTCACTGT GCCCCATCCC AACATCGAGG AGGTTGCTCT GTCCACCACC GGAGAGATCC CTTTTTACGG
      GGAGGCCCCGA GGCAGTGACA CGGGGTAGGG TTGTAGCTCC TCCAACGAGA CAGGTGGTGG CCTCTCTAGG GAAAAATGCC


+2    K  A  I    P  L  E  V    I  K  G    G  R  H    L  I  F  C    H  S  K    K  K  C    D  E  L
2401  CAAGGCTATC CCCCTCGAAG TAATCAAGGG GGGGAGACAT CTCATCTTCT GTCATTCAAA GAAGAAGTGC GACGAACTCG
      GTTCCGATAG GGGGAGCTTC ATTAGTTCCC CCCCTCTGTA GAGTAGAAGA CAGTAAGTTT CTTCTTCACG CTGCTTGAGC


+2    A  A  K  L    V  A  L    G  I  N  A    V  A  Y    Y  R  G    L  D  V  S    V  I  P    T  S  G
2481  CCGCCAAAGCT GGTCGCATTG GGCATCAATG CCGTGGCCTA CTACCGCGGT CTTGACGTGT CCGTCATCCC GACCAGCGGC
      GGCGGTTTCGA CCAGCGTAAC CCGTAGTTAC GGCACCGGAT GATGGCGCCA GAACTGCACA GGCAGTAGGG CTGGTCGCCG
```

FIG. 5-Page 4

pCMV-delNS35

```
     +2  G  A  K  D    V  R  C    H  A  R  K    A  V  T    H  I  N    S    V  W  K    D  L  L    E  D  N
5841     GGGCAAAAGA CGTCCGTTGC CATGCCAGAA AGGCCGTAAC CCACATCAAC TCCGTGTGGA AAGACCTTCT GGAAGACAAT
         CCCGTTTTCT GCAGGCAACG GTACGGTCTT TCCGGCATTG GGTGTAGTTG AGGCACACCT TTCTGGAAGA CCTTCTGTTA
```

```
     +2  V  T  P  I    D  T  T    I  M  A    K  N  E  V    F  C  V    Q  P  E    K  G  G  R    K  P  A
5921     GTAACACCAA TAGACACTAC CATCATGGCT AAGAACGAGG TTTTCTGCGT TCAGCCTGAG AAGGGGGGTC GTAAGCCAGC
         CATTGTGGTT ATCTGTGATG GTAGTACCGA TTCTTGCTCC AAAAGACGCA AGTCGGACTC TTCCCCCCAG CATTCGGTCG
```

```
     +2  R  L  I    V  F  P  D    L  G  V    R  V  C    E  K  M  A    L  Y  D    V  V  T    K  L  P
6001     TCGTCTCATC GTGTTCCCCG ATCTGGGCGT GCGCGTGTGC GAAAAGATGG CTTTGTACGA CGTGGTTACA AAGCTCCCT
         AGCAGAGTAG CACAAGGGGC TAGACCCGCA CGCGCACACG CTTTTCTACC GAAACATGCT GCACCAATGT TTCGAGGGGA
```

```
     +2  L  A  V  M    G  S  S    Y  G  F  Q    Y  S  P    G  G  Q  R    V  E  F  L    V  Q  A    W  K  S
6081     TGGCCGTGAT GGGAAGCTCC TACGGATTCC AATACTCACC AGGACAGCGG GTTGAATTCC TCGTGCAAGC GTGGAAGTCC
         ACCGGCACTA CCCTTCGAGG ATGCCTAAGG TTATGAGTGG TCCTGTCGCC CAACTTAAGG AGCACGTTCG CACCTTCAGG
                                                                       EcoRI
                                                                       - - - - - - - -
```

```
     +2  K  K  T  P    M  G  F    S  Y  D    T  R  C  F    D  S  T    V  T  E    S  D  I  R    T  E  E
6161     AAGAAAACCC CAATGGGGTT CTCGTATGAT ACCCCGCTGCT TTGACTCCAC AGTCACTGAG AGCGACATCC GTACGGAGGA
         TTCTTTTGGG GTTACCCCAA GAGCATACTA TGGGCGACGA AACTGAGGTG TCAGTGACTC TCGCTGTAGG CATGCCTCCT
```

```
     +2  A  I  Y    Q  C  C  D    L  D  P    Q  A  R    V  A  I  K    S  L  T    E  R  L    Y  V  G
6241     GGCAATCTAC CAATGTGTGTG ACCTCGACCC CCAAGCCCGC GTGGCCATCA AGTCCCTCAC CGAGAGGCTT TATGTTGGGG
         CCGTTAGATG GTTACACACAC TGGAGCTGGG GGTTCGGGCG CACCGGTAGT TCAGGGAGTG GCTCTCCGAA ATACAACCCC
```

```
     +2  G  P  L  T    N  S  R    G  E  N  C    G  Y  R    R  C  R    A  S  G  V    L  T  T    S  C  G
6321     GCCCTCTTAC CAATTCAAGG GGGAGAACT GCGGCTATCG CGGCTGCCGC CAGGTGCCGG GCGAGCGGCG TACTGACAAC TAGCTGTGGT
         CGGGAGAATG GTTAAGTTCC CCCTCTTGA CGCCGATAGC GCCGACGGCG GTCCACGGCC CGCTCGCCGC ATGACTGTTG ATCGACACCA
```

FIG. 5-Page 11

pCMV-deINS35

```
+2
        S T L     S T A L     A E L     A T R     S F G   S     S S T     S G I     T G D
5281    ATCAACCCTA TCTACTGCCT TGGCCGAGCT AGCTTTGGCA GCTCCTCAAC TTCCGGCATT ACGGGGGACA
        TAGTTGGGAT AGATGACGGA ACCGGCTCGA TCGAAACCGT CGAGGAGTTG AAGGCCGTAA TGCCCCGTGT


+2
        N T T     S S E     P A P S     G C P     P D S     D A E S     Y S S     M P P
5361    ATACGACAAC ATCCTCTGAG CCCGCCCCTT CTGGCTGCCC CCCCGACTCC GACGCTGAGT CCTATTCCTC CATGCCCCCC
        TATGCTGTTG TAGGAGACTC GGGCGGGGAA GACCGACGGG GGGGCTGAGG CTGCGACTCA GGATAAGGAG GTACGGGGGG


+2
        L E G E     P G D     P D L     S D G S     W       S T V S S     E A N A     E D V
                              BamHI

5441    CTGGAGGGGG AGCCTGGCCA TCCGGATCTT AGCGACGGGT CATGGTCAAC GGTCAGTAGT GAGGCCAACG CGGAGGATGT
        GACCTCCCCC TCGGACCGGT AGGCCTAGAA TCGCTGCCCA GTACCAGTTG CCAGTCATCA CTCCGGTTGC GCCTCCTACA


+2
        V C C     S M S Y     S W T     G A L     V T P C     A A E     E Q K     L P I
5521    CGTGTGCTGC TCAATGTCTT ACTCTTGGAC AGGCGCCACTC GTCACCCCGT GGGCGGGCA AGAAACAGAAA CTGCCCATCA
        GCACACGACG AGTTACAGAA TGAGAACCTG TCCGCGGTGAG CAGTGGGGCA CCGGCGGCCT TCTTGTCTTT GACGGGTAGT


+2
        N A L S     N S L     L R H H     N L V     Y S T     T S R S     A C Q     R Q K
5601    ATGGCACTAAG CAACTCGTTG CTACGTCACC ACAATTTGGT GTATTCCACC ACCTCACCCA GTGCTTGCCA AAGGCAGAAG
        TACCGTGATTC GTTGAGCAAC GATGCAGTGG TGTTAAACCA CATAAGGTGG TGGAGTGGGT CACGAACGGT TTCCGTCTTC


+2
        K V T F     D R L     Q V L     D S H Y     Q D V     L K E     V K A A     A S K
5681    AAAGTCACAT TTGACAGACT GCAAGTTCTG GACAGCCATT ACCAGGACGT ACTCAAGGAG GTTAAAGCAG CGGCGGTCAAA
        TTTCAGTGTA AACTGTCTGA CGTTCAAGAC CTGTCGGTAA TGGTCCTGCA TGAGTTCCTC CAATTTCGTC GCCGCCAGTTT


+2
        V K A     N L L S     V E E     A C S     L P P     H S A     K S K     F G Y
5761    AGTGAAGGCT AACTTGCTAT CCGTAGAGGA AGCTTGCAGC CTGACGCCCC CACACTCAGC CAAATCCAAG TTTGGTTATG
        TCACTTCCGA TTGAACGATA GGCATCTCCT TCGAACGTCG GACTGCGGGG GTGTGAGTCG GTTTAGGTTC AAACCAATAC
```

FIG. 5–Page 10

pCMV-delNS35

```
     +2  L  H  E  Y  P  V  G  S  Q  L  P  C  E  P  E  P  D  V  A  V  L  T  S  M  L  T  D
4721     CTCCACGAAT ACCCGGTAGG GTCCCAATTA CCTTGCCGAGC CCGAACCCGA CGTGGCCCGTG TTGACGTCCA TGCTCACTGA
         GAGGTGCTTA TGGGCCATCC CAGGGTTAAT GGAACGGCTCG GGCTTGGGCCT GCACCGGCAC AACTGCAGGT ACGAGTGACT

     +2  P  S  H  I  T  A  E  A  A  G  R  R  L  A  R  G  S  P  P  S  V  A  S  S  S  A
4801     TCCCTCCCAT ATAACAGCAG AGGCGGCCGG GCGAAGGTTG GCGAGGGGGAT CACCCCCCTC TGTGGCCAGC TCCTCGGCTA
         AGGGAGGGTA TATTGTCGTC TCCGCCGGCC CGCTTCCAAC CGCTCCCCTA GTGGGGGGAG ACACCGGTCG AGGAGCCGAT

     +2  S  Q  L  S  A  P  S  L  K  A  T  C  T  A  N  H  D  S  P  D  A  E  L  I  E  A  N
4881     GCCAGCTATC CGCTCCATCT CTCAAGGCAA CTTGCCACCGC TAACCATGAC TCCCCTGATG CTGAGCTCAT AGAGGCCAAC
         CGGTCGATAG GCGAGGTAGA GAGTTCCGTT GAACGTGGCG ATTGGTACTG AGGGGACTAC GACTCGAGTA TCTCCGGTTG

     +2  L  L  W  R  Q  E  M  G  G  N  I  T  R  V  E  S  E  N  K  V  V  I  L  D  S  F  D
4961     CTCGCTATGGA GGCGAGGAGAT GGGCGGCCAAC ATCACCAGGG TTGAGTCAGA AAACAAAGTG GTGATTCTGG ACTCCTTCGA
         GAGGATACCT CCGCTCCTCTA CCCGCCGGTTG TAGTGGTCCC AACTCAGTCT TTTGTTTCAC CACTAAGACC TGAGGAAGCT

     +2  P  L  V  A  E  E  D  E  R  E  I  S  V  P  A  E  I  L  R  K  S  R  R  F  A  Q
5041     TCCGGCTTGTG GCGGAGGAGGA ACGAGGGGGA GATCTCGCCGTA CCCGCAGAAA TCCTGCGCAA GTCTCGGGAGA TTCGCCCAGG
         AGGCCGAACAC CGCCTCCTCC TGCTCGCCCT CTAGAGCGGAT GGGCGTCTTT AGGACGCCTT CAGAGCCCTCT AAGCGGGTCC

     +2  A  L  P  V  W  A  R  P  D  Y  N  P  P  L  V  E  T  W  K  K  P  D  Y  E  P  P  V
5121     CCCTGCCCGT TTGGGCGCGG CCGGACTATA ACCCCCCCGCT AGTGGAGACG TGGAAAAAGC CCGACTACGA ACCACCTGTG
         GGGACGGGCA AACCCGCGCC GGCCTGATAT TGGGGGGGCGA TCACCTCTGC ACCTTTTTCG GGCTGATGCT TGGTGGACAC

     +2  V  H  G  C  P  L  P  P  P  K  S  P  P  V  P  P  P  R  K  K  R  T  V  V  L  T  E
5201     GTCCATGGCT GCCCGGCTTCC ACCTCCAAAG TCCCCTCCTG TGCCTCCCGCC TCGGAAGAAG CGGACGGTGG TCCTCACTGA
         CAGGTACCGA CGGGCCGAAGG TGGAGGTTTC AGGGGAGGAC ACGGAGGGCGG AGCCTTCTTC GCCTGCCACC AGGAGTGACT
```

FIG. 5-Page 9

pCMV-II
4276 bp

*Eco*R I (1983)

Xba I (2002)

*Bam*H I (2028)

Mlu I (2037)
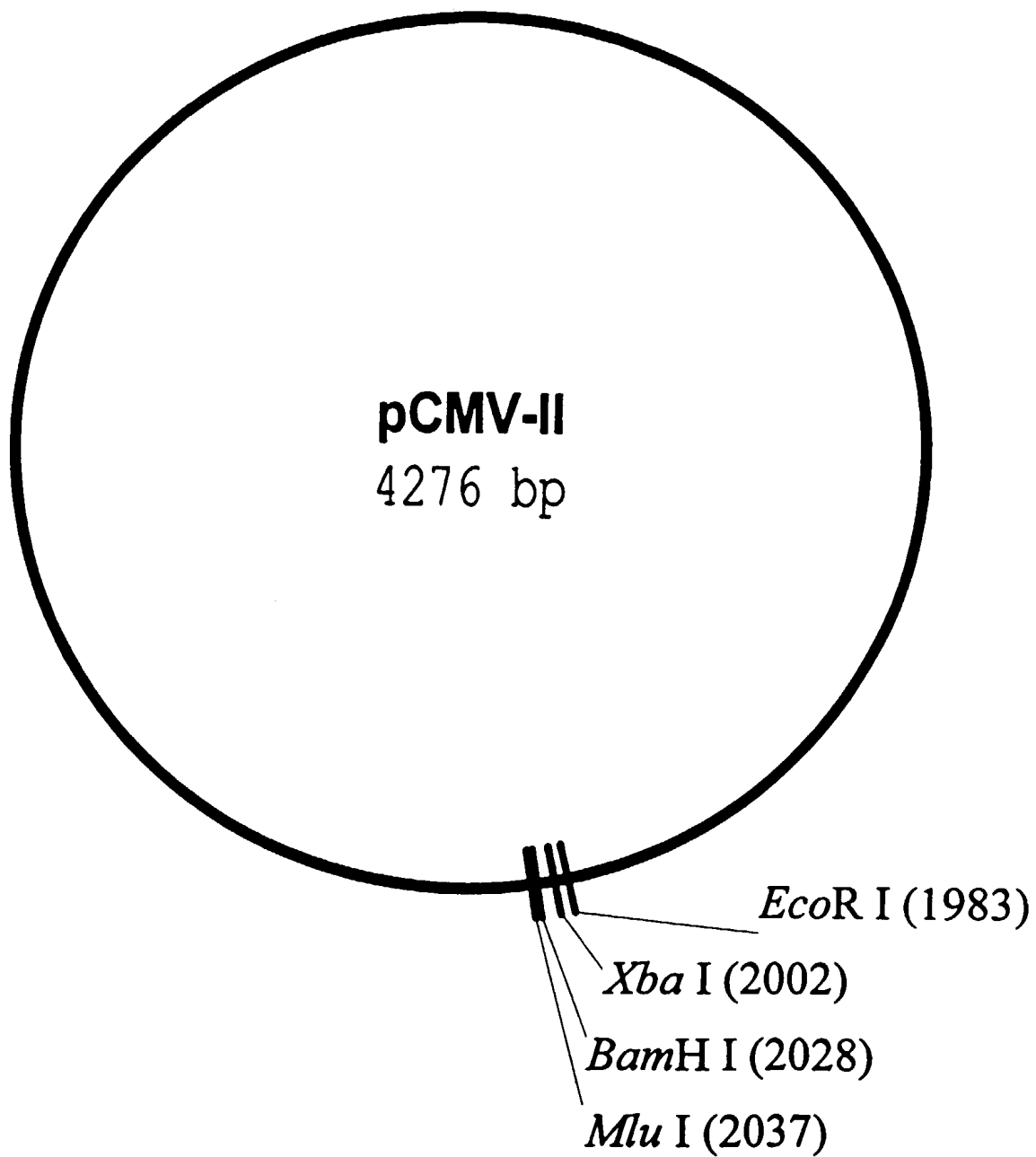
FIG. 6

pCMV-delNS35

8961 CCCATGTTGT GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT
GGGTACAACA CGTTTTTTCG CCAATCGAGG AAGCCAGGAG GCTAGCAACA GTCTTCATTC AACCGGCGTC ACAATAGTGA

9041 CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT GAGTACTCAA
GTACCAATAC CGTCGTGACG TATTAAGAGA ATGACAGTAC GGTAGGCATT CTACGAAAAG ACACTGACCA CTCATGAGTT

9121 CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG CTCTTGCCCG GCGTCAATAC GGGATAAATAC CGCGCCACAT
GGTTCAGTAA GACTCTTATC ACATACGCCG CTGGCTCAAC GAGAACGGGC CCCTATTATG GCGCGGTGTA

9201 AGCAGAACTT TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTTGAGATC
TCGTCTTGAA ATTTTCACGA GTAGTAACCT TTTGCAAGAA GCCCCGCTTT TGAGAGTTCC TAGAATGGCG ACAACTCTAG

9281 CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTCA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA
GTCAAGCTAC ATTGGGTGAG CACGTGGGTT GACTAGAAGT CGTAGAAAAT GCAAAGACCC ACTCGTTTTT

9361 CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT TGAATACTCA TACTCTTCCT TTTTCAATAT
GTCCTTCCGT TTTACGGCGT TTTTTCCCTT ATTCCCGCTG TGCCTTTACA ACTTATGAGT ATGAGAAGGA AAAAGTTATA

9441 TATTGAAGCA TTTATCAGGG TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT
ATAACTTCGT AAATAGTCCC AATAACAGAG TACTCGCCTA TGTATAAACT TACATAAATC TTTTTATTTG TTTATCCCCA

9521 TCCGCGCCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA TTATCATGAC ATTAACCTAT AAAAATAGGC
AGGCGCGGTGT AAAGGGGCTT TTCACGGTGG ACTGCAGATT AATAGTACTG TAATTGGATA TTTTTATCCG

9601 GTATCACGAG GCCCTTTCGT C
CATAGTGCTC CGGGAAAGCA G

FIG. 5-Page 16

pCMV-delNS35

```
        +2  I  S  S  E    C  T  T    P  C  S  G    S  W  L    R  D  I    W  D  W    I    C  E  V    L  S  D
        4161  TAAGCTCGGA  GTGTACCACT  CCATGCTCCG  GTTCCTGGCT  AAGGGACATC  TGGGACTGGA  TATGGCGAGT  GTTGAGCGGAC
              ATTCGAGCCT  CACATGGTGA  GGTACGAGGC  CAAGGACCGA  TTCCCTGTAG  ACCCTGACCT  ATACGCTCCA  CAACTCGCTG

        +2  F  K  T  W    L  K  A    K  L  M    P  Q  L  P    G  I  P    F  V  S    C  Q  R  G    Y  K  G
        4241  TTTAAGACCT  GGCTAAAAGC  TAAGCTCATG  CCACAGCTGC  CTGGGATCCC  CTTTGTGTCC  TGCCAGCGCG  GGTATAAAGGG
              AAATTCTGGA  CCGATTTTCG  ATTCGAGTAC  GGTGTCGACG  GACCCTAGGG  GAAACACAGG  ACGGTCGCGC  CCATATTTCCC
                                                      BamHI
                                                      -----

        +2  V  W  R    G  D  G  I    M  H  T    R  C  H    C  G  A  E    I  T  G    H  V  K    N  G  T
        4321  GGTCTGGCGA  GGGGACGGCA  TCATGCACAC  TCGCTGCCAC  TGTGGAGCTG  AGATCACTGG  ACATGTCAAA  AACGGGACGA
              CCAGACCGCT  CCCCTGCCGT  AGTACGTGTG  AGCGACGGTG  ACACCTCGAC  TCTAGTGACC  TGTACAGTTT  TTGCCCTGCT

        +2  M  R  I  V    G  P  R    T  C  R  N    M  W  S    G  T  F    P  I  N  A    Y  T  T    G  P  C
        4401  TCAGGATCGT  CGGTCCTAGG  ACCTGCAGGA  ACATGTGGAG  TGGGACCTTC  CCCATTAATG  CCTACACCAC  GGGCCCCTGT
              AGTCCTAGCA  GCCAGGATCC  TGGACGTCCT  TGTACACCTC  ACCCTGGAAG  GGGTAATTAC  GGATGTGGTG  CCCGGGGACA

        +2  T  P  L  P    A  P  N    Y  T  F    A  L  W  R    V  S  A    E  E  Y    V  E  I  R    Q  V  G
        4481  ACCCCCCTTC  CTGCGCCCAA  CTACACGTTC  GCGCTATGGA  GGGTGTCTGC  AGAGGAATAC  GTGGAGATAA  GGCAGGTGGG
              TGGGGGGAAG  GACGCGGGTT  GATGTGCAAG  CGCGATACCT  CCCACAGACG  TCTCCTTATG  CACCTCTATT  CCGTCCACCC

        +2  D  F  H    Y  V  T  G    M  T  T    D  N  L    K  C  P  C    Q  V  P    S  P  E    F  F  T
        4561  GGACTTCCAC  TACGTGACGG  GTATGACTAC  TGACAATCTT  AAATGCCCGT  GCCAGGTCCC  ATCGGCCCGAA  TTTTTCACAG
              CCTGAAGGTG  ATGCACTGCC  CATACTGATG  ACTGTTAGAA  TTTACGGGCA  CGGTCCAGGG  TAGCCGGGCTT  AAAAAGTGTC

        +2  E  L  D  G    V  R  L    H  R  F  A    P  P  C    K  P  L    L  R  E  E    V  S  F    R  V  G
        4641  AATTGGACGG  GGTGCGCCTA  CATAGGTTTG  CGCCCCCCTG  CAAGCCCCTG  CTGCGGGGAGG  AGGTATCATT  CAGAGTAGGA
              TTAACCTGCC  CCACGCGGAT  GTATCCAAAC  GCGGGGGGAC  GTTCGGGGAC  GACGCCCCTCC  TCCATAGTAA  GTCTCATCCT
```

FIG. 5-Page 8

```
1361   CTCTATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT GACACCGGACT CTGTATTTTT ACAGGGATGGG GTCCATTTAT
       GAGATAACCG ATATACGGTT ATGAGACAGG AAGTCTCTGA CTGTGCCTGA GACATAAAAA TGTCCTACCC CAGGTAAATA

1441   TATTTACAAA TTCACATATA CAACAACGCC GTCCCCCGTG CCCGCAGTTT TTATTAAACA TAGCGGTGGGA TCTCCGACAT
       ATAAATGTTT AAGTGTATAT GTTGTTGCGG CAGGGGGCAC GGGCGTCAAA AATAATTGT ATCGCCACCCT AGAGGCTGTA

1521   CTCGGGTACG TGTTCCGGAC ATGGGCTCTT CTCGGGTAGC GGCGGAGCTT CCACATCCGA GCCCTGGTCC CATCCGTCCA
       GAGCCCATGC ACAAGGCCTG TACCCGAGAA GAGCCCATCG CCGCCTCGAA GGTGTAGGCT CGGGACCAGG GTAGGCAGGT

1601   GCGGCTCATG GTCGCTCGGC AGCTCCTTGC TCCTAACAGT GGAGGCCCAGA CTTAGGCACA GCACAATGCC CACCACCACC
       CGCCGAGTAC CAGCCGAGCCG TCGAGGAACG AGGATTGTCA CCTCCGGTCT GAATCCGTGT CGTGTTACGG GTGGTGGTGG

1681   AGTGTGCCGC ACAAGGCCGT GGCGGTAGGG TATGTGTCTG AAAATGAGCT CGGAGATTGG GCTCGCCACCT GGACCCAGAT
       TCACACGGCG TGTTCCGGCA CCGGCCATCCC ATACACAGAC TTTTACTCGA GCCTCTAACC CGAGCGGTGGA CCTGCGTCTA

1761   GGAAGACTTA AGGCAGCGGC AGAAGAAGAT GCAGGCAGCT GAGTTGTTGT ATTCTGATAA GAGTCAGAGG TAACTCCCGT
       CCTTCTGAAT TCCGTCGCCG TCTTCTTCTA CGTCCGTCGA CTCAACAACA TAAGACTATT CTCAGTCTCC ATTGAGGGCA

1841   TGCGGTGCTG TTAACGGTGG AGGGCAGTGT AGTCTGAGCA GTACTCGTTG CTGCCGCGCG CGCCACCAGA CATAAATAGCT
       ACGCCACGAC AATTGCCACC TCCCGTCACA TCAGACTCGT CATGAGCAAC GACGGCGCGC GCGGTGGTCT GTATTATCGA

       +2                                                              M   A   A

                                                          EcoRI
                                                          -----
1921   GACAGACTAA CAGACTGTTC CTTTCCATGG GTCTTTTCTG CAGTCACCGT CGTCGACCTA AGAATTCACC ATGGCTGCAT
       CTGTCTGATT GTCTGACAAG GAAAGGTACC CAGAAAGAC GTCAGTGGCA GCAGCTGGAT TCTTAAGTGG TACCGACGTA
```

FIG. 5-Page 3

pCMV-delNS35

```
641  AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTCCGCCC CCTATTGACG TCAATGACGG TAAATGGCCC
     TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCAGGCGGG GGATAACTGC AGTTACTGCC ATTTACCGGG

721  GCCTGGCATT ATGCCCAGTA CATGACCTTA CGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC
     CGGACCGTAA TACGGGTCAT GTACTGGAAT GCCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG

801  CATGGTGATG CGGTTTTGGC AGTACACCAA TGGGCGTGGA TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA
     GTACCACTAC GCCAAAACCG TCATGTGGTT ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT

881  TTGACGTCAA TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ATAACCCCGC CCCGTTGACG
     AACTGCAGTT ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TATTGGGGCG GGGCAACTGC

961  CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG
     GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC

1041 CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCGGGGCCG GGAACGGTGC ATTGGAACGC
     GGTAGGTGCG ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGCCCCGGC CCTTGCCACG TAACCTTGCG

1121 GGATTCCCCG TGCCAAGAGT GACGTAACTA CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCCTAT GCATGCTATA
     CCTAAGGGGC ACGGTTCTCA CTGCATTGAT GGCGGATATC TGAGATATCC GTGTGGGGAA ACCGAGGATA CGTACGATAT

1201 CTGTTTTTGG CTTGGGGCCT ATACACCCCC GCTCCTTATG CTATAGGTGA TGGTATAGCT TAGCCTATAG GTGTGGGTTA
     GACAAAAACC GAACCCCGGA TATGTGGGGG CGAGGAATAC GATATCCACT ACCATATCGA ATCGGATATC CACACCCAAT

1281 TTGACCATTA TTGACCACTC CCCTATTGGT GACGATACTT TCCATTACTA ATCCATAAACA TGGCTCTTTG CCACAACTAT
     AACTGGTAAT AACTGGTGAG GGGATAACCA CTGCTATGAA AGGTAATGAT TAGGTATTGT ACCGAGAAAC GGTGTTGATA
```

FIG. 5-Page 2

```
      +2       L   S   T       L   P   G   N       P   A   I       A   S   L       M   A   F   T       A   A   V       T   S   P       L   T   T
    3601    CTGTCAACG CTGCCTGGTA ACCCCGCCAT TGCTTCATTG ATGGCTTTTA CAGCTGCTGT CACCAGCCCA CTAACCACTA
            GAACAGTTGC GACGGACCAT TGGGGCGGTA ACGAAGTAAC TACCGAAAAT GTCGACGACA GTGGTCGGGT GATTGGTGAT

      +2       S   Q   T   L       L   F   N       I   L   G   G       W   V   A       A   Q   L       A   A   P   G       A   A   T       A   F   V
    3681    GCCAAACCCT CCTCTTCAAC ATATTGGGGG GGTGGGTGGC TGCCCAGCTC GCCGCCCCCG GTGCCGCTAC TGCCTTTGTG
            CGGTTTGGGA GGAGAAGTTG TATAACCCCC CCACCCACCG ACGGGTCGAG CGGCGGGGGC CACGGCGATG ACGGAAACAC

      +2       G   A   G   L       A   G   A       A   I   G       S   V   G   L       G   K   V       L   I   D       I   L   A   G       Y   G   A
    3761    GGGGCTGGCT TAGCTGGCGC CGCCATCGGC AGTGTTGGAC TGGGGAAGGT CCTCATAGAC ATCCTTGCAG GGTATGGCGC
            CCCGCGACCGA ATCGACCGCG GCGGTAGCCG TCACAACCTG ACCCCTTCCA GGAGTATCTG TAGGAACGTC CCATACCGCG

      +2       G   V   A       G   A   L   V       A   F   K       I   M   S       G   E   V   P       S   T   E       D   L   V       N   L   L
    3841    GGGGCTGGCG GGAGCTCTTG TGGCATTCAA GATCATGAGC GGTGAGGTCC CCTCCACGGA GGACCTGGTC AATCTACTGC
            CCCCGACCGC CCTCGAGAAC ACCGTAAGTT CTAGTACTCG CCACTCCAGG GGAGGTGCCT CCTGGACCAG TTAGATGACG

      +2       P   A   I   L       S   P   G       A   L   V   V       G   V   V       C   A   A       I   L   R   R       H   V   G       P   G   E
    3921    CCGGCCATCCT CTCGCCCCGGA GCCCTCGTAG TCGGGGTGGT CTGTGCCAGCA ATACTGCGCC GGCACGTTGG CCCGGGGCGAG
            GGGCCGGTAGGA GAGCGGGGCCT CGGGAGCATC AGCCCCACCA GACACGGTCGT TATGACGCGG CCGTGCAACC GGGCCCCGCTC

      +2       G   A   V   Q       W   M   N       R   L   I       A   F   A   S       R   G   N       H   V   S       P   T   H   Y       V   P   E
    4001    GGGGCAGTGC AGTGGATGAA CCGGCTGATA GCCTTCGCCT CCCGGGGCGAA CCATGTTTCC CCCACGGCACT AGTGCCGGA
            CCCCGTCACG TCACCTACTT GGCCGACTAT CGGAAGCGGA GGGCCCCCTT GGTACAAAGG GGGTGCCGTGA TGCACGGCCT

      +2       S   D   A       A   A   R   V       T   A   I       L   S   S       L   T   V   T       Q   L   L       R   R   L       H   Q   W
    4081    GAGCGGATGCA GCTGCCCGCG TCACTGCCAT ACTCAGCAGC CTCACTGTAA CCCAGCTCCT GAGGCGACTG CACCAGTGGA
            CTCGCCTACGT CGACGGGCGC AGTGACGGTA TGAGTCGTCG GAGTGACATT GGGTCGAGGA CTCCGCTGAC GTGGTCACCT
```

FIG. 5-Page 7

pCMV-deINS35

```
  1  TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT
     AGCGCGCAAA GCCACTACTG CCACTTTTGG AGACTGTGTA CGTCGAGGGC CTCTGCCAGT GTCGAACAGA CATTCGCCTA

 81  GCCGGGAGCA GACAAGCCCG TCAGGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA
     CGGCCCTCGT CTGTTCGGGC AGTCCCCGCGC AGTCGCCCAC AGCCCCGACC      GAATTGATAC GCCGTAGTCT

                                                         StuI
                                                         -----
161  GCAGATTGTA CTGAGAGTGC ACCATATGAA GCTTTTTGCA AAAGCCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG
     CGTCTAACAT GACTCTCACG TGGTATACTT CGAAAAACGT TTTCGGATCC GGAGGTTTTT TCGGAGGAGT GATGAAGACC

241  AATAGCTCAG AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGGGGGCGGAG ATTGGGCGGA
     TTATCGAGTC TCCGGCTCCG CCGGAGCCGG AGACGTATTT ATTTTTTTTA ATCAGTCGGT ACCCCGCCTC TTACCCGCCT

321  ACTGGGCGGG GAGGGAATTA TTGGCTATTG GCCATTGCAT ACGTTGTATC TATATCATAA TATGTACATT TATATTGGCT
     TGACCCGCCC CTCCCTTAAT AACCGATAAC CGGTAACGTA TGCAACATAG ATATAGTATT ATACATGTAA ATATAACCGA

401  CATGTCCAAT ATGACCGCCA TGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT
     GTACAGGTTA TACTGGCGGT ACAACTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA

481  AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCATT
     TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGCGGGTAA

561  GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT
     CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTC ATAAATGCCA
```
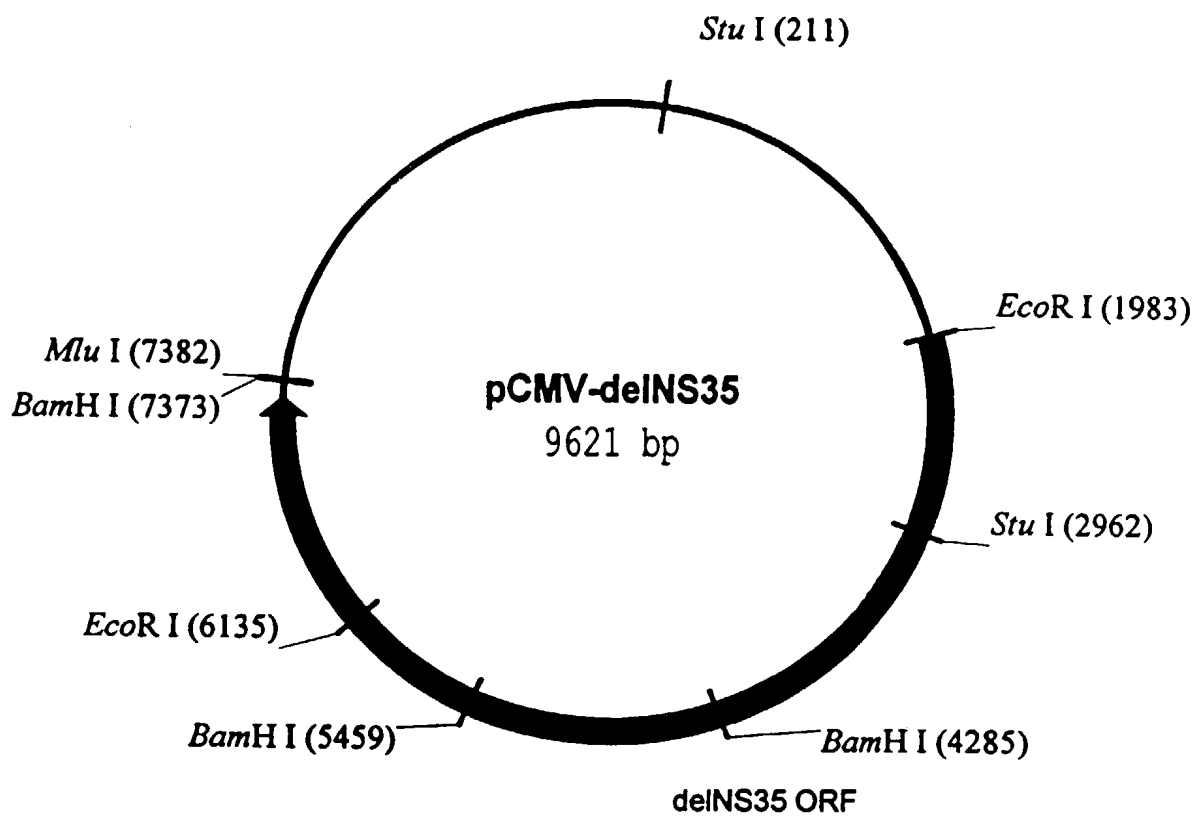
FIG. 5-Page 1

Stu I (211)

EcoR I (1983)

Mlu I (7382)
*Bam*H I (7373)

pCMV-delNS35
9621 bp

Stu I (2962)

EcoR I (6135)

*Bam*H I (5459)

*Bam*H I (4285)

delNS35 ORF

FIG. 4

```
+2
3041  A  T  V  C  A  R  A   Q  A  P   P  P  S  W  D  Q  M   W  K  C   L  I  R  L   K  P  T
      GCCACCGTGT GCGCTAGGGC TCAAGCCCCT CCCCCATCGT GGGACCAGAT GTGGAAGTGT TTGATTCGCC TCAAGCCCAC
      CGGTGGCACA CGCGATCCCG AGTTCGGGGA GGGGGTAGCA CCCTGGTCTA CACCTTCACA AACTAAGCGG AGTTCGGGTG

+2
3121  L  H  G   P  T  P  L   L  Y  R   L  G  A   V  Q  N  E  I  T  L   T  H  P   V  T  K
      CCTCCATGGG CCAACACCCC TGCTATACAG ACTGGGCGCT GTTCAGAATG AAATCACCCT GACGCACCCA GTCACCAAAT
      GGAGGTACCC GGTTGTGGGG ACGATATGTC TGACCCGCGA CAAGTCTTAC TTTAGTGGGA CTGCGTGGGT CAGTGGTTTA

+2
3201  Y  I  M  T   C  M  S   A  D  L  E  V  V  T   S  T  W   V  L  V  G   G  V  L   A  A  L
      ACATCATGAC ATGCATGTCG GCCGACCTGG AGGTCGTCAC GAGCACCTGG GTGCTCGTTG GGCCCGTCCT GGCTGCTTTG
      TGTAGTACTG TACGTACAGC CGGCTGGACC TCCAGCAGTG CTCGTGGACC CACGAGCAAC CCGGCCAGGA CCGACGAAAC

+2
3281  A  A  Y  C  L  S  T   G  C  V   V  I  V  G   R  V  V   L  S  G   K  P  A  I   I  P  D
      GCCGCGTATT GCCTGTCAAC AGGCTGCGTG GTCATAGTGG GCAGGGTCGT CTTGTCCGGG AAGCCCGCAA TCATACCTGA
      CGGCGCATAA CGGACAGTTG TCCGACGCAC CAGTATCACC CGTCCCAGCA GAACAGGCCC TTCGGGCGTT AGTATGGACT

+2
3361  R  E  V   L  Y  R  E  F  D  E   M  E  E   C  S  Q  H   L  P  Y   I  E  Q   G  M  M
      CAGGGAAGTC CTCTACCGAG AGTTCGATGA GATGGAAGAG TGCTCTCAGC ACTTACCGTA CATCGAGCAA GGGATGATGC
      GTCCCTTCAG GAGATGGCTC TCAAGCTACT CTACCTTCTC ACGAGAGTCG TGAATGGCAT GTAGCTCGTT CCCTACTACG

+2
3441  L  A  E  Q   F  K  Q   K  A  L  G   L  L  Q   T  A  S   R  Q  A  E   V  I  A   P  A  V
      TCGCCGACCA GTTCAAGCAG AAGGCCCTCG GCCTCCTGCA GACCGCCGTCC CGTCAGGCAG AGGTTATCGC CCCTGCTGTC
      AGCGGCTGGT CAAGTTCGTC TTCCGGGAGC CGGAGGACGT CTGGCGGCAGG GCAGTCCGTC TCCAATAGCG GGGACGACAG

+2
3521  Q  T  N  W   Q  K  L   E  T  F   W  A  K  H  M  W  N   F  I  S   G  I  Q  Y   L  A  G
      CAGACCAACT GGCAAAAACT CGAGACCTTC TGGGCGAAGC ATATGTGGAA CTTCATCAGT GGGATACAAT ACTTGGCGGG
      GTCTGGTTGA CCGTTTTTGA GCTCTGGAAG ACCCGCTTCG TATACACCTT GAAGTAGTCA CCCTATGTTA TGAACCGCCC
```

FIG. 5-Page 6

pCMV-delNS35

```
        D  V  V  V  V  A  T   D  A  L   M  T  G  Y   T  G  D   F  D  S   V  I  D  C  N  T  C
+2
2561  GATGTTGTCG TCGTGGCAAC CGATGCCCTC ATGACCGGCT ATACCGGGGA CTTCGACTCG GTGATAGACT GCAATACCTG
      CTACAACAGC AGCACCGTTG GCTACGGGAG TACTGGCCGA TATGGCCCGA GAAGCTGAGC CACTATCTGA CGTTATGCAC

        V  T  Q   T  V  D  F   S  L  D   P  T  F   T  I  E  T   I  T  L   P  Q  D   A  V  S
+2
2641  TGTCACCCAG ACAGTCGATT TCAGCCTTGA CCCTACCTTC ACCATTGAGA CAATCACGCT CCCCCAAGAT GCTGTCTCCC
      ACAGTGGGTC TGTCAGCTAA AGTCGGAACT GGGATGGAAG TGGTAACTCT GTTAGTGCGA GGGGGTTCTA CGACAGAGGG

        R  T  Q  R   R  G  R   T  G  R  G   K  P  G   I  Y  R   F  V  A  P   G  E  R   P  S  G
+2
2721  GCACTCAACG TCGGGGCCAGG ACTGGCCAGG GGAAGCCAGG CATCTACAGA TTTGTGGCAC CGGGGGGAGCG CCCCTCCGGC
      CGTGAGTTGC AGCCCCGTCC TGACCGGTCC CCTTCGGTCC GTAGATGTCT AAACACCGTG GCCCCCTCGC GGGGAGGCCG

        M  F  D  S   S  V  L   C  E  C   Y  D  A  G   C  A  W   Y  E  L   T  P  A  E   T  T  V
+2
2801  ATGTTCGACT CGTCCGTCCT CTGTGAGTGC TATGACGCAG GCTGCTGCTG GTATGAGCTC ACGCCCGCCG AGACTACAGT
      TACAAGCTGA GCAGGCAGGA GACACTCACG ATACTGCGTC CGACGACGAC CATACTCGAG TGCGGGCGGC TCTGATGTCA

        R  L  R   A  Y  M  N   T  P  G   L  P  V   C  Q  D  H   L  E  F   W  E  G   V  F  T
+2                                                                                     StuI
                                                                                     --
2881  TAGGCTACGA GCGGTACATGA ACACCCCGGG GCTTCCCGTG TGCCAGGACC ATCTTGAATT TTGGGAGGGC GTCTTTACAG
      ATCCGATGCT CGCCATGTACT TGTGGGGCCC CGAAGGGCAC ACGGTCCTGG TAGAACTTAA AACCCTCCCG CAGAAATGTC

        G  L  T  H   I  D  A   H  F  L  S   Q  T  K   Q  S  G   E  N  L  P   Y  L  V   A  Y  Q
+2      StuI
        ----
2961  GCCTCACTCA TATAGATGCC CACTTTCTAT CCCAGACAAA GCAGAGTGGG GAGAACCTTC CTTACCTGGT AGGCTACCAA
      CGGAGTGAGT ATATCTACGG GTGAAAGATA GGGTCTGTTT CGTCTCACCC CTCTTGGAAG GAATGGACCA TCGCATGGTT
```

FIG. 5-Page 5

pCMV-NS35

8961 CCCATGTTGT GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAG TGTTATCACT
      GGGTACAACA CGTTTTTTCG CCAATCGAGG AAGCCAGGAG GCTAGCAACA GTCTTCATTC AACCGGCGTC ACAATAGTGA

9041 CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT GAGTACTCAA
      GTACCAATAC CGTCGTGACG TATTAAGAGA ATGACAGTAC GGTAGGCATT CTACGAAAAG ACACTGACCA CTCATGAGTT

9121 CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG CTCTTGCCCG GCGTCAATAC GGGATAATAC CGCGCCACAT
      GGTTCAGTAA GACTCTTATC ACATACGCCG CTGGCTCAAC GAGAACGGGC CGCAGTTATG CCCTATTATG GCGCGGTGTA

9201 AGCAGAACTT TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTTGAGATC
      TCGTCTTGAA ATTTTCACGA GTAGTAACCT TTTGCAAGAA GCCCCGCTTT TGAGAGTTCC TAGAATGGCG ACAACTCTAG

9281 CAGTTCGATG TAACCCACTC GTGCACCCAA CTGATCTTTA GCATCTTTTA CTTTCACCAG CGTTTCTGGG TGAGCAAAAA
      GTCAAGCTAC ATTGGGTGAG CACGTGGGTT GACTAGAAGT CGTAGAAAAT GAAAGTGGTC GCAAAGACCC ACTCGTTTTT

9361 CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT TGAATACTCA TACTCTTCCT TTTTCAATAT
      GTCCTTCCGT TTTACGGCGT TTTTTCCCTT ATTCCCGCTG TGCCTTTACA ACTTATGAGT ATGAGAAGGA AAAAGTTATA

9441 TATTGAAGCA TTTATCAGGG TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT
      ATAACTTCGT AAATAGTCCC AATAACAGAG TACTCGCCTA TGTATAAACT TACATAAATC TTTTTATTTG TTTATCCCCA

9521 TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCTAA GAAACCATTA TTATCATGAC ATTAACCTAT AAAAATAGGC
      AGGCGCGTGT AAAGGGGCTT TTCACGGTGG ACTGCAGATT CTTTGGTAAT AATAGTACTG TAATTGGATA TTTTTATCCG

9601 GTATCACGAG GCCCTTTCGT C
      CATAGTGCTC CGGGAAAGCA G

FIG. 3-Page 16

```
8241  AGGACAGTAT TTGGTATCTG CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA
      TCCTGTCATA AACCATAGAC GCGAGACGAC TTCGGTCAAT GGAAGCCTTT TTCTCAACCA TCGAGAACTA GGCCGTTTGT

8321  AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT
      TTGGTGGCGA CCATCGCCAC CAAAAAAACA AACGTTCGTC GTCTAATGCG CGTCTTTTTT TCCTAGAGTT CTTCTAGGAA

8401  TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG
      ACTAGAAAAG ATGCCCCAGA CTGCGAGTCA CCTTGCTTTT GAGTGCAATT CCCTAAAACC AGTACTCTAA TAGTTTTTCC

8481  ATCTTCACCT AGATCCTTTT AAATTAAAAA TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG
      TAGAAGTGGA TCTAGGAAAA TTTAATTTTT ACTTCAAAAT TTAGTTAGAT TTCATATATA CTCATTTGAA CCAGACTGTC

8561  TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC GTTCATCCAT AGTTGCCTGA CTCCCCGTCG
      AATGGTTACG AATTAGTCAC TCCGTGGATA GAGTCGCTAG ACAGATAAAG CAAGTAGGTA TCAACGGACT GAGGGGCAGC

8641  TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG CTCACCGGCT
      ACATCTATTG ATGCTATGCC CTCCCGAATG GTAGACCGGG GTCACGACGT TACTATGGCG CTCTGGGTGC GAGTGGCCGA

8721  CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA
      GGTCTAAATA GTCGTTATTT GGTCGGTCGG CCTTCCCGGC TCGCGTCTTC ACCAGGACGT TGAAATAGGC GGAGGTAGGT

8801  GTCTATTAAT TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA CGTTGTTGCC ATTGCTACAG
      CAGATAATTA ACAACGGCCC TTCGATCTCA TTCATCAAGC GGTCAATTAT CAAACGCGTT GCAACAACGG TAACGATGTC

8881  GCATCGTGGT GTCACGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC
      CGTAGCACCA CAGTGCGAGC AGCAAACCAT ACCGAAGTAA GTCGAGGCCA AGGGTTGCTA GTTCCGCTCA ATGTACTAGG
```

FIG. 3-Page 15

pCMV-NS35

7521 CGCATTGTCT GAGTAGGTGT CATTCTATTC TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGAGGGATTG GGAAGACAAT
      GCGTAACAGA CTCATCCACA GTAAGATAAG ACCCCCCACC CCACCCCGTC CTGTCGTTCC CCTCGTTAAC CCTTCTGTTA

7601 AGCAGGCATG CTGGGGAGCT CTTCCGCTTC CTCGCTCACT GACTCGGCTGC GCTCGGTCGT TCGGCTGCGG CGAGCGGTAT
      TCGTCCGTAC GACCCCTCGA GAAGGCGAAG GAGCGAGTGA CTGAGCCGACG CGAGCCAGCA AGCCGACGCC GCTCGCCATA

7681 CAGCTCACTC AAAGGCGGTA ATACGGTTAT CCACAGAATC AGGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG
      GTCGAGTGAG TTTCCGCCAT TATGCCAATA GGTGTCTTAG TCCCCTATTG CGTCCTTTCT TGTACACTCG TTTTCCGGTC

7761 CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA
      GTTTTCCGGT CCTTGGCATT TTTCCGGCGC AAAAGGTATC CGAGGCGGGG GGACTGCTCG TAGTGTTTTT

7841 TCGACGCTCA AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC TCCCTCGTGC
      AGCTGCGAGT TCAGTCTCCA CCGCTTTGGG CTGTCCTGAT ATTTCTATGG TCCGCAAAGG GGGACCTTCG AGGGAGCACG

7921 GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC
      CGAGAGGACA AGGCTGGGAC GGCGAATGGC CTATGGACAG GCGGAAAGAG GGAAGCCCTT CGCACCGCGA AAGAGTTACG

8001 TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA
      AGTGCGACAT CCATAGAGTC AAGCCACATC CAGCAAGCGA GGTTCGACCC GACACACGTG CTTGGGGGGC AAGTCGGGCT

8081 CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG
      GGCGACGCGG AATAGGCCAT TGATAGCAGA ACTCAGGTTG GGCCATTCTG TGCTGAATAG CGGTGACCGT CGTCGGTGAC

8161 GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG AAGTGGTGGC CTAACTACGG CTACACTAGA
      CATTGTCCTA ATCGTCTCGC TCCATACATC CGCCACGATG TCTCAAGAAC TTCACCACCG GATTGATGCC GATGTGATCT

FIG. 3-Page 14

pCMV-NS35

```
     +2  N   T   T   S   S   E   P   A   P   S   G   C   P   P   D   S   D   A   E   S   Y   S   S   M   P   P
    5361  ATACGACAAC ATCCTCTGAG CCCGCCCCTT CTGGCTGCCC CCCGACTCC GACGCTGAGT CCTATTCCTC CATGCCCCCC
          TATGCTGTTG TAGGAGACTC GGGCGGGGAA GACCGACGGG GGGGCTGAGG CTGCGACTCA GGATAAGGAG GTACGGGGGG
```

```
     +2  L   E   G   E   P   G   D   P   D   L   S   D   G   S   W   S   T   V   S   S   E   A   N   A   E   D   V
    5441  CTGGAGGGG AGCCTGGGGA TCCGGATCTT AGCGACGGGT CATGGTCAAC GGTCAGTAGT GAGGCCAACG CGGAGGATGT
              BamHI
          GACCTCCCCC TCGGACCCCT AGGCCTAGAA TCGCTGCCCA GTACCAGTTG CCAGTCATCA CTCCGGTTGC GCCTCCTACA
```

```
     +2  V   C   C   S   M   S   Y   S   W   T   G   A   L   V   T   P   C   A   A   E   E   Q   K   L   P   I
    5521  CGTGTGCTGC TCAATGTCTT ACTCTTGGAC AGGGCCACTC GTCACCCCGT GCGCCGCGGA AGAAACAGAAA CTGCCCATCA
          GCACACGACG AGTTACAGAA TGAGAACCTG TCCGGTGAG CAGTGGGGCA CGCGGCGCCT TCTTGTCTTT GACGGGTAGT
```

```
     +2  N   A   L   S   N   S   L   L   R   H   H   N   L   V   Y   S   T   T   S   R   S   A   C   Q   R   Q   K
    5601  ATGCACTAAG CAACTCGTTG CTACGTCACC ACAATTTGGT GTATTCCACC ACCTCACGCA GTGCTTGCCA AAGGCAGAAG
          TACGTGATTC GTTGAGCAAC GATGCAGTGG TGTTAAACCA CATAAGGTGG TGGAGTGCGT CACGAACGGT TTCCGTCTTC
```

```
     +2  K   V   T   F   D   R   L   Q   V   L   D   S   H   Y   Q   D   V   L   K   E   V   K   A   A   A   S   K
    5681  AAAGTCACAT TTGACAGACT GCAAGTTCTG GACAGCCATT ACCAGGACGT ACTCAAGGAG GTTAAAGCAG CGGCGGTCAAA
          TTTCAGTGTA AACTGTCTGA CGTTCAAGAC CTGTCGGTAA TGGTCCTGCA TGAGTTCCTC CAATTTCGTC GCCGCCAGTT
```

```
     +2  V   K   A   N   L   L   S   V   E   E   A   C   S   L   T   P   P   H   S   A   K   S   K   F   G   Y
    5761  AGTGAAGGCT AACTTGCTAT CCGTAGAGGA AGCTTGCAGC CTCACGCCCC CACACTCAGC CAAATCCAAG TTTGGTTATG
          TCACTTCCGA TTGAACGATA GGCATCTCCT TCGAACGTCG GAGTGCGGGG GTGTGAGTCG GTTTAGGTTC AAACCAATAC
```

FIG. 3–Page 10

pCMV-NS35

```
          S   P   G   E   I   N   R   V   A   A   C   L   R   K   L   G   V   P   P   L   R   A   W   R   H   R
+2
6961  CTCTCCAGGT GAAATCAATA GGGTGGCCGC ATGCCTCAGA AAACTTGGGG TACCGCCCT GCGAGCTTGG AGACACCGGG
      GAGAGGTCCA CTTTAGTTAT CCCACCGGCG TACGGAGTCT TTTGAACCCC ATGGCGGGAA CGCTCGAACC TCTGTGGCCC

          A   R   S   V   R   A   R   L   L   A   R   G   G   R   A   A   I   C   G   K   Y   L   F   N   W   A   V
+2
7041  CCCGGAGCGT CCGCGCTAGG CTTCTGGCCA GAGGAGGCAG GGCTGCCATA TGTGGCAAGT ACCTCTTCAA CTGGGCAGTA
      GGGCCTCGCA GGCGCGATCC GAAGACCGGT CTCCTCCGTC CCGACGGTAT ACACCGTTCA TGGAGAAGTT GACCCGTCAT

          R   T   K   L   T   P   I   A   A   A   G   Q   L   D   L   S   G   W   F   T   A   G   Y   S   G
+2
7121  AGAACAAAGC TCAAACTCAC TCCAATAGCG GCCGCTGGCC AGCTGGACTT GTCCGGCTGG TTCACGGCTG GCTACAGCGG
      TCTTGTTTCG AGTTTGAGTG AGGTTATCGC CGGCGACCGG TCGACCTGAA CAGGCCGACC AAGTGCCGAC CGATGTCGCC

          G   D   I   Y   H   S   V   S   H   A   R   P   R   W   I   W   F   C   L   L   L   L   A   G   V
+2
7201  GGGAGACATT TATCACAGCG TGTCTCATGC CCGGCCCCGC TGGATCTGGT TTTGCCTACT CCTGCTTGCT GCAGGGGTAG
      CCCTCTGTAA ATAGTGTCGC ACAGAGTACG GGCCGGGGCG ACCTAGACCA AAACGGATGA GGACGAACGA CGTCCCCATC

          G   I   Y   L   L   P   N   R
+2
7281  GCATCTACCT CCTCCCCAAC CGATGAAGGT TGGGGTAAAC ACTCCGGCCT AAAAAAAAAA AAAAATCTAG AAAGGGCGGC
      CGTAGATGGA GGAGGGGTTG GCTACTTCCA ACCCCATTTG TGAGGCCGGA TTTTTTTTTT TTTTTAGATC TTTCCGCCG

          BAMHI     MluI
          -----     -----
7361  CAAGATATCA AGGATCCACT ACGCGGTTAGA GCTCGCTGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT
      GTTCTATAGT TCCTAGGTGA TGCGCCAATCT CGAGCGACTA GTCGGAGCTG ACACGGAAGA TCAACGGTCG GTAGACAACA

7441  TTGCCCCTCC CCGTGCCT  CCTTGACCCT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAAATGAG GAAATTGCAT
      AACGGGGAGG GGCACGGAA  GGAACTGGGA CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC CTTTAACGTA
```

FIG. 3-Page 13

pCMV-NS35

```
     N  T  L  T  C  Y  I  K  A  R   A  A  C  R  A  A  G   L  Q  D   C  T  M  L   V  C  G
+2
6401 AACACCCTCA CTTGCTACAT CAAGGCCCGG GCAGCCTGTC GAGCCGCAGG GCTCCAGGAC TGCACCATGC TCGTGTGTGG
     TTGTGGGAGT GAACGATGTA GTTCCGGGCC CGTCGGACAG CTCGGCGTCC CGAGGTCCTG ACGTGGTACG AGCACACACC


     D  D  L   V  V  I  C   E  S  A   G  V  Q   E  D  A  A   S  L  R   A  F  T   E  A  M
+2
6481 CGACGACTTA GTCGTTATCT GTGAAAGCGC GGGGGTCCAG GAGGACGCGG CGAGCCTTCACG GAGGCTATGA
     GCTGCTGAAT CAGCAATAGA CACTTTCGCG CCCCCAGGTC CTCCTGCGCC GCTCGGAAGTGC CTCCGATACT


     T  R  Y  S   A  P  P   G  D  P  P   Q  P  E   Y  D  L   E  L  I  T   S  C  S   S  N  V
+2
6561 CCAGGTACTC CGCCCCCCCT GGGGACCCCC CACAACCAGA ATACGACTTG GAGCTCATAA CATCATGTCG CTCCAACGTG
     GGTCCATGAG GCGGGGGGGA CCCCTGGGGG GTGTTGGTCT TATGCTGAAC CTCGAGTATT GTAGTACAGC GAGGTTGCAC


     S  V  A  H   D  G  A   G  K  R   V  Y  Y  L   T  R  D   P  T  T   P  L  A  R   A  A  W
+2
6641 TCAGTCGCCC ACGACGGCGC TGGAAAGAGG GTCTACTACC TCACCCGTGA CCCTACAACC CCCTCGCCGA GAGCTGCGTG
     AGTCAGCGGG TGCTGCCGCG ACCTTTCTCC CAGATGATGG AGTGGGCACT GGGAGCGGCT CTCGACGCAC


     E  T  A   R  H  T  P   V  N  S   W  L  G   N  I  I  M   F  A  P   T  L  W   A  R  M
+2
6721 GGAGACAGCA AGACACACTC CAGTCAATTC CTGGCTAGGC AACATAATCA TGTTTGCCCC CACACTGTGG GCGAGGATGA
     CCTCTGTCGT TCTGTGTGAG GTCAGTTAAG GACCGATCCG TTGTATTAGT ACAAACGGGG GTGTGACACC CGCTCCTACT


     I  L  M  T   H  F  F   S  V  L  I   A  R  D   Q  L  E   Q  A  L  D   C  E  I   Y  G  A
+2
6801 ATTGATGAC CCATTTCTTT AGCGTCCTTA TAGCCAGGA CCAGCTTGAA CAGGCCCCTCG ATTGGCGAGAT CTACGGGGCC
     TAACTACTG GGTAAAGAAA TCGCAGGAAT ATCGGTCCCT GTCGGAACTT GTCCGGGGAGC TAACGCTCTA GATGCCCCGG


     C  Y  S  I   E  P  L   D  L  P   P  I  I  Q   R  L  H   G  L  S   A  F  S  L   H  S  Y
+2
6881 TGCTACTCCA TAGAACCACT GGATCTACCT CCAATCATTC AAAGACTCCA TGGCCTCAGC GCATTTTCAC TCCACAGTTA
     ACGATGAGGT ATCTTGGTGA CCTAGATGGA GGTTAGTAAG TTTCTGAGGT ACCGGAGTCG CGTAAAAGTG AGGTGTCAAT
```

FIG. 3-Page 12

pCMV-NS35

```
    P  S  H   I  T  A  E   A  A  G   R  R  L   A  R  G   S  P  P  S   V  A  S   S  S  A
+2  TCCCTCCCAT ATAACAGCAG AGGCGGCCGG GCGAAGGTTG GCGAGGGGAT CACCCCCCTC TGTGGCCAGC TCCTCGGCTA
4801 AGGGAGGGTA TATTGTCGTC TCCGCCGGCC CGCTTCCAAC CGCTCCCCTA GTGGGGGGAG ACACCGGTCG AGGAGCCGAT

    S  Q  L  S   A  P  S   L  K  A  T   C  T  A   N  H  D   S  P  D  A   E  L  I   E  A  N
+2  GCCAGCTATC CGCTCCCATCT CTCAAGGCAA CTTGCCACCGC TAACCATGAC TCCCCTGATG CTGAGCTCAT AGAGGCCAAC
4881 CGGTCGATAG GCGAGGTAGA GAGTTCCGTT GAACGGTGGCG ATTGGTACTG AGGGGACTAC GACTCGAGTA TCTCCGGTTG

    L  L  W  R   Q  E  M   G  G  N   I  T  R  V   E  S  E   N  K  V   V  I  L  D   S  F  D
+2  CTCCTATGGA GGCAGGAGAT GGGGCGCAAC ATCACCAGGG TTGAGTCAGA AAACAAAGTG GTGATTCTGG ACTCCTTCGA
4961 GAGGATACCT CCGTCCTCTA CCCGCCGTTG TAGTGGTCCC AACTCAGTCT TTTGTTTCAC CACTAAGACC TGAGGAAGCT

    P  L  V   A  E  E  D   E  R  E   I  S  V   P  A  E  I   L  R  K   S  R  R   F  A  Q
+2  TCCGCTTGTG GCGGAGGAGG ACGAGCGGGA GATCTCCGTA CCCGCAGAAA TCCTGCGGAA GTCTCGGAGA TTCGCCCAGG
5041 AGGCGAACAC CGCCTCCTCC TGCTCGCCCT CTAGAGGCAT GGGCGTCTTT AGGACGCCTT CAGAGCCTCT AAGCGGGTCC

    A  L  P  V   W  A  R   P  D  Y  N   P  P  L   V  E  T   W  K  K  P   D  Y  E   P  P  V
+2  CCCTGCCCGT TTGGGCGCGG CCGGACTATA ACCCCCCGCT AGTGGAGACG TGGAAAAAGC CCGACTACGA ACCACCTGTG
5121 GGGACGGGCA AACCCGCGCC GGCCTGATAT TGGGGGGCGA TCACCTCTGC ACCTTTTTCG GGCTGATGCT TGGTGGACAC

    V  H  G  C   P  L  P   P  P  K   S  P  P  V   P  P  P   R  K  K   R  T  V  V   L  T  E
+2  GTCCATGGCT GCCCGCTTCC ACCTCCAAAG TCCCCTCCTG TGCCTCCGCC TCGGAAGAAG CGGACGGTGG TCCTCACTGA
5201 CAGGTACCGA CGGGCGAAGG TGGAGGTTTC AGGGGAGGAC ACGGAGGCGG AGCCTTCTTC GCCTGCCACC AGGAGTGACT

    S  T  L   S  T  A  L   A  T  R   S  F  G  S   S  S  T   S  G  I   T  G  D
+2  ATCAACCCTA TCTACTGCCT TGGCCGAGCT CGCCACCAGA AGCTTTGGCA GCTCCTCAAC TTCCGGCATT ACGGGCGACA
5281 TAGTTGGGAT AGATGACGGA ACCGGCTCGA GCGGTGGTCT TCGAAACCGT CGAGGAGTTG AAGGCCGTAA TGCCCGCTGT
```

FIG. 3-Page 9

pCMV-NS35

+2 F K T W L K A K L M P Q L P G I P F V S C Q R G Y K G
                                                           BamHI

4241 TTTAAGACCT GGCTAAAAGC TAAGCTCATG CCACAGCTGC CTGGGATCCC CTTTGTGTCC TGCCAGCGCG GGTATAAGGG
      AAATTCTGGA CCGATTTTCG ATTCGAGTAC GGTGTCGACG GACCCTAGGG GAAACACAGG ACGGTCGCGC CCATATTCCC

+2   V W R   G D G I M H T   R C H   C G A E   I T G   H V K   N G T
4321 GGTCTGGCGA GGGGACGGCA TCATGCACAC TCGCTGCCAC TGTGGAGCTG AGATCACTGG ACATGTCAAA AACGGGACGA
      CCAGACCGCT CCCCTGCCGT AGTACGTGTG AGCGACGGTG ACACCTCGAC TCTAGTGACC TGTACAGTTT TTGCCCTGCT

+2   M R I V   G P R   T C R N M W S   G T F   P I N A   Y T T   G P C
4401 TGAGGATCGT CGGTCCTAGG ACCTGCAGGA ACATGTGGAG TGGGACCTTC CCCATTAATG CCTACACCAC GGGCCCCTGT
      ACTCCTAGCA GCCAGGATCC TGGACGTCCT TGTACACCTC ACCCTGGAAG GGGTAATTAC GGATGTGGTG CCCGGGGACA

+2   T P L P A P N   Y T F   A L W R   V S A   E E Y   V E I R   Q V G
4481 ACCCCCCTTC CTGCGCCCAA CTACACGTTC GGGCTATGGA GGGTGTCTGC AGAGGAATAC GTGGAGATAA GGCAGGTGGG
      TGGGGGGAAG GACGCGGGTT GATGTGCAAG CCCGATACCT CCCACAGACG TCTCCTTATG CACCTCTATT CCGTCCACCC

+2   D F H   Y V T G   M T T   D N L   K C P C Q V P   S P E   F F T
4561 GGACTTCCAC TACGTGACGG GTATGACTAC TGACAATCTT AAATGCCCGT GCCAGGTCCC ATCGCCCGAA TTTTTCACAG
      CCTGAAGGTG ATGCACTGCC CATACTGATG ACTGTTAGAA TTTACGGGCA CGGTCCAGGG TAGCGGGCTT AAAAAGTGTC

+2   E L D G   V R L   H R F A   P P C   K P L   L R E E   V S F   R V G
4641 AATTGGACGG GGTGCGCCTA CATAGGTTTG CGCCCCCCTG CAAGCCCCTG CTGCGGGAGG AGGTATCATT CAGAGTAGGA
      TTAACCTGCC CCACGCGGAT GTATCCAAAC GCGGGGGGAC GTTCGGGGAC GACGCCCTCC TCCATAGTAA GTCTCATCCT

+2   L H E Y P V G   S Q L   P C E P E P D   V A V   L T S M L T D
4721 CTCCACGAAT ACCCGGTAGG GTCGCAATTA CCTTGCCGAGC CCGAACCCGGA CGTGGCCGTG TTGACGTCCA TGCTCACTGA
      GAGGTGCTTA TGGGCCATCC CAGCGTTAAT GGAACGGCTCG GGCTTGGGCCT GCACCGGCAC AACTGCAGGT ACGAGTGACT

FIG. 3-Page 8

pCMV-NS35

+2
```
     S   Q   T   L   L   F   N   I   L   G   G   W   V   A   A   Q   L   A   A   P   G   A   A   T   A   F   V
3681 GCCAAACCCT CCTCTTCAAC ATATTGGGGG GGTGGGTGGC TGCCCAGCTC GCCGCCCCCG GTGCCCTTGTG
     CGGTTTGGGA GGAGAAGTTG TATAACCCCC CCACCCACCG ACGGGTCGAG CGGCGGGGGC CACGGGAAACAC
```

+2
```
     G   A   G   L   A   G   A   A   I   G   S   V   G   L   G   K   V   L   I   D   I   L   A   G   Y   G   A
3761 GGCGGCTGGCT TAGCTGGCGC CGCCATCGGC AGTGTTGGAC TGGGGAAGGT CCTCATAGAC ATCCTTGCAG GGTATGGCGC
     CCGCCGACCGA ATCGACCGCG GCGGTAGCCG TCACAACCTG ACCCCTTCCA GGAGTATCTG TAGGAACGTC CCATACCGCG
```

+2
```
     G   V   A   G   A   L   V   A   F   K   I   M   S   G   E   V   P   S   T   E   D   L   V   N   L
3841 GGGCGTGGCG GGAGCTCTTG TGGCATTCAA GATCATGAGC GGTGAGGTCC CCTCCACGGA GGACCTGGTC AATCTACTGC
     CCCGCACCGC CCTCGAGAAC ACCGTAAGTT CTAGTACTCG CCACTCCAGG GGAGGTGCCT CCTGGACCAG TTAGATGACG
```

+2
```
     P   A   I   L   S   P   G   A   L   V   V   G   V   V   C   A   A   I   L   R   R   H   V   G   P   G   E
3921 CCGGCCATCCT CTCGCCCGGA GCCCTCGTAG TCGGCGTGGT CTGTGCCGCA ATACTGCGCC GGCACGTTGG CCCGGGCGAG
     GGCCGGTAGGA GAGCGGGCCT CGGGAGCATC AGCCGCACCA GACACGGCGT TATGACGCGG CCGTGCAACC GGGCCCGCTC
```

+2
```
     G   A   V   Q   W   M   N   R   L   I   A   F   A   S   R   G   N   H   V   S   P   T   H   Y   V   P   E
4001 GGGGCAGTGC AGTGGATGAA CCGGCTGATA GCCTTCGCCT CCCGGGGGAA CCATGTTTCC CCCACCGCACT ACGTGCCGGA
     CCCCGTCACG TCACCTACTT GGCCGACTAT CGGAAGCGGA GGGCCCCCTT GGTACAAAGG GGGTGGCGTGA TGCACGGCCT
```

+2
```
     S   D   A   A   R   V   T   A   I   L   S   S   L   T   V   T   Q   L   L   R   R   L   H   Q   W
4081 GAGCGGATGCA GCTGCCCGCG TCACTGCCAT ACTCAGCAGC CTCACTGTAA CCCAGCTCCT GAGGGGACTG CACCAGTGGA
     CTCGCCTACGT CGACGGGCGC AGTGACGGTA TGAGTCGTCG GAGTGACATT GGGTCGAGGA CTCCGCTGAC GTGGTCACCT
```

+2
```
     I   S   S   E   C   T   T   P   C   S   G   S   W   L   R   D   I   W   D   W   I   C   E   V   L   S   D
4161 TAAGCTCGGA GGTGTACCACT CCATGCTCCG GTTCCTGGCT AAGGGACATC TGGGACTGGA TATGCGAGGT GTTGAGCGAC
     ATTCGAGCCT CACATGGTGA GGTACGAGGC CAAGGACCGA TTCCCTGTAG ACCCTGACCT ATACGCTCCA CAACTCGCTG
```

FIG. 3-Page 7

pCMV-NS35

```
+2       L  H  G      P  T  P  L  L  Y  R      L  G  A      V  Q  N  E      I  T  L      T  H  P      V  T  K
3121   CCTCCATGGG CCAAGACCCC TGCTATACAG ACTGGGCGCT GTTCAGAATG AAATCACCCT GACGCACCCA GTCACCAAAT
       GGAGGTACCC GGTTCTGGGG ACGATATGTC TGACCCGCGA CAAGTCTTAC TTTAGTGGGA CTGCGTGGGT CAGTGGTTTA


+2       Y  I  M  T      C  M  S      A  D  L  E      V  V  T      S  T  W      V  L  V  G      G  V  L      A  A  L
3201   ACATCATGAC ATGCATGTCG GCCGACCTGG AGGTCGTCAC GAGCACCTGG GTGCTCGTTG GCGGGGTCCT GGCTGCTTTG
       TGTAGTACTG TACGTACAGC CGGCTGGACC TCCAGCAGTG CTCGTGGACC CACGAGCAAC CGCCCCAGGA CCGACGAAAC


+2       A  A  Y  C      L  S  T      G  C  V      V  I  V  G      R  V  V      L  S  G      K  P  A  I      I  P  D
3281   GCCGCGTATT GCCTGTCAAC AGGCTGCGTG GTCATAGTGG GCAGGGTCGT CTTGTCCGGG AAGCCGGCAA TCATACCTGA
       CGGCGCATAA CGGACAGTTG TCCGACGCAC CAGTATCACC CGTCCCAGCA GAACAGGCCC TTCGGCCGTT AGTATGGACT


+2       R  E  V      L  Y  R  E      F  D  E      M  E  E      C  S  Q  H      L  P  Y      I  E  Q      G  M  M
3361   CAGGGAAGTC CTCTACCGAG AGTTCGATGA GATGGAAGAG TGCTCTCAGC ACTTACCGTA CATCGAGCAA GGGATGATGC
       GTCCCTTCAG GAGATGGCTC TCAAGCTACT CTACCTTCTC ACGAGAGTCG TGAATGGCAT GTAGCTCGTT CCCTACTACG


+2       L  A  E  Q      F  K  Q      K  A  L  G      L  L  Q      T  A  S      R  Q  A  E      V  I  A      P  A  V
3441   TCGGCCGAGCA GTTCAAGCAG AAGGCCCTCG GCCTCCTGCA GACCGCGTCC CGTCAGGCAG AGGTTATCGC CCCTGCTGTC
       AGCCGGCTCGT CAAGTTCGTC TTCCGGGAGC CGGAGGACGT CTGGCGCAGG GCAGTCCGTC TCCAATAGCG GGGACGACAG


+2       Q  T  N  W      Q  K  L      E  T  F      W  A  K  H      M  W  N      F  I  S      G  I  Q  Y      L  A  G
3521   CAGACCAACT GGCAAAAACT CGAGACCTTC TGGGCGAAGC ATATGTGGAA CTTCATCAGT GGGATACAAT ACTTGGCGGG
       GTCTGGTTGA CCGTTTTTGA GCTCTGGAAG ACCCGCTTCG TATACACCTT GAAGTAGTCA CCCTATGTTA TGAACCGCCC


+2       L  S  T      L  P  G  N      P  A  I      A  S  L      M  A  F  T      A  A  V      T  S  P      L  T  T
3601   CTTGTCAACG CTGCCTGGTA ACCCCGCCAT TGCTTCATTG ATGGCTTTTA CAGCTGCTGT CACCAGCCCA CTAACCACTA
       GAACAGTTGC GACGGACCAT TGGGGCGGTA ACGAAGTAAC TACCGAAAAT GTCGACGACA GTGGTCGGGT GATTGGTGAT
```

FIG. 3-Page 6

```
     +2  V  T  Q   T  V  D  F   S  L  D   P  T  F   T  I  E  T   I  I  T  L   P  Q  D   A  V  S
    2641 TGTCACCCAG ACAGTCGATT TCAGCCTTGA CCCTACCTTC ACCATTGAGA CAATCACGCT CCCCCAAGAT GCTGTCTCCC
         ACAGTGGGTC TGTCAGCTAA AGTCGGAACT GGGATGGAAG TGGTAACTCT GTTAGTGCGA GGGGGTTCTA CGACAGAGGG

     +2  R  T  Q  R   R  G  R   T  G  R  G   K  P  G   I  Y  R   F  V  A  P   G  E  R   P  S  G
    2721 GCACTCAACG TCGGGGCAGG ACTGGGCAGG GGAAGCCAGG CATCTACAGA TTTGTGGCAC CGGGGGGAGCG CCCCTCCGGC
         CGTGAGTTGC AGCCCCGTCC CCTTCGGTCC GTAGATGTCT AAACACCGTG GCCCCCCTCGC GGGGAGGCCG

     +2  M  F  D  S   S  V  L   C  E  C   Y  D  A  G   C  A  W   Y  E  L   T  P  A  E   T  T  V
    2801 ATGTTCGACT CGTCCGTCCT CTGTGAGTGC TATGACGCAG GCTGTGCTTG GTATGAGCTC ACGCCCGCCG AGACTACAGT
         TACAAGCTGA GCAGGCAGGA GACACTCACG ATACTGCGTC CGACACGAAC CATACTCGAG TGCGGGCGGC TCTGATGTCA

     +2  R  L  R   A  Y  M  N   T  P  G   L  P  V   C  Q  D  H   L  E  F   W  E  G   V  F  T
                                                                                         StuI
                                                                                         --
    2881 TAGGCTACGA GCGTACATGA ACACCCCGGG GCTTCCCGTG TGCCAGGACC ATCTTGAATT TTGGGAGGGC GTCTTTACAG
         ATCCGATGCT CGCATGTACT TGTGGGGCCC CGAAGGGCAC ACGGTCCTGG TAGAACTTAA AACCCTCCCG CAGAAATGTC

     +2  G  L  T   H  I  D  A   H  F  L  S   Q  T  K   Q  S  G   E  N  L  P   Y  L  V   A  Y  Q
         StuI
         ----
    2961 GCCTCACTCA TATAGATGCC CACTTTCTAT CCCAGACAAA GCAGAGTGGG GAGAACCTTC CTTACCTGGT AGCGTACCAA
         CGGAGTGAGT ATATCTACGG GTGAAAGATA GGGTCTGTTT CGTCTCACCC CTCTTGGAAG GAATGGACCA TCGCATGGTT

     +2  A  T  V  C   A  R  A   Q  A  P   P  P  S  W   D  Q  M   W  K  C   L  I  R  L   K  P  T
    3041 GCCACCGTGT GGGCTAGGGC TCAAGCCCCT CCCCCATCGT GGGACCAGAT GTGGAAGTGT TTGATTCGCC TCAAGCCCAC
         CGGTGGCACA CCCGATCCCG AGTTCGGGGA GGGGGTAGCA CCCTGGTCTA CACCTTCACA AACTAAGCGG AGTTCGGGTG
```

FIG. 3-Page 5

```
     +2  A  H  G  I   D  P  N    I  R  T    G  V  R  T    I  T  T    G  S  P     I  T  Y  S    T  Y  G
2081     GCTCATGGGA  TCGATCCTAA  CATCAGGACC  GGGGTGAGAA  CAATTACCAC  TGGCAGCCCC  ATCACGTACT  CCACCTACGG
         CGAGTACCCT  AGCTAGGATT  GTAGTCCTGG  CCCCACTCTT  GTTAATGGTG  ACCGTCGGGG  TAGTGCATGA  GGTGGATGCC

     +2  K  F  L    A  D  G  G    C  S  G    G  A  Y    D  I  I    I  C  D  E    C  H  S     T  D  A
2161     CAAGTTCCTT  GCCGACGGCG  GGTGCTCGGG  GGGGCCTTAT  GACATAATAA  TTTGTGACGA  GTGCCACTCC  ACGGATGCCA
         GTTCAAGGAA  CGGCTGCCGC  CCACGAGCCC  CCCCGGAATA  CTGTATTATT  AAACACTGCT  CACGGTGAGG  TGCCTACGGT

     +2  T  S  I  L    G  I  G    T  V  L  D    Q  A  E    T  A  G    A  R  L    V  V  L  A     T  A  T
2241     CATCCATCTT  GGGCATTGGC  ACTGTCCTTG  ACCAAGCAGA  GACTGCGGGG  GCGAGACTGG  TTGTGCTCGC  CACCGCCACC
         GTAGGTAGAA  CCCGTAACCG  TGACAGGAAC  TGGTTCGTCT  CTGACGCCCC  CGCTCTGACC  AACACGAGCG  GTGGCGGTGG

     +2  P  P  G  S    V  T  V    P  H  P    N  I  E  E    V  A  L    S  T  T    G  E  I  P    F  Y  G
2321     CCTCCGGGCT  CCGTCACTGT  GCCCCATCCC  AACATCGAGG  AGGTTGCTCT  GTCCACCACC  GGAGAGATCC  CTTTTTACGG
         GGAGGCCCGA  GGCAGTGACA  CGGGGTAGGG  TTGTAGCTCC  TCCAACGAGA  CAGGTGGTGG  CCTCTCTAGG  GAAAAATGCC

     +2  K  A  I    P  L  E  V    I  K  G    G  R  H    L  I  F  C    H  S  K  K  C    D  E  L
2401     CAAGGCTATC  CCCCTCGAAG  TAATCAAGGG  GGGAGAGACAT  CTCATCTTCT  GTCATTCAAA  GAAGAAGTGC  GACGAACTCG
         GTTCCGATAG  GGGGAGCTTC  ATTAGTTCCC  CCCCTCTGTA  GAGTAGAAGA  CAGTAAGTTT  CTTCTTCACG  CTGCTTGAGC

     +2  A  A  K  L    V  A  L    G  I  N  A    V  A  Y    Y  R  G    L  D  V  S    V  I  P    T  S  G
2481     CCGCAAAGCT  GGTCGCCATTG  GCCATCAATG  CCGTGGCCTA  CTACCGCGGT  CTTGACGTGT  CCGTCATCCC  GACCAGCGGC
         GGCGTTTCGA  CCAGCGGTAAC  CGGTAGTTAC  GGCACCGGAT  GATGGCGCCA  GAACTGCACA  GGCAGTAGGG  CTGGTCGCCG

     +2  D  V  V  V  A  T    D  A  L    M  T  G  Y    T  G  D    F  D  S     V  I  D  C  N  T  C
2561     GATGTTGTCG  TCGTGGCAAC  CGATGCCCTC  ATGACCGGCT  ATACCGGCGA  CTTCGACTCG  GTGATAGACT  GCAATACGTG
         CTACAACAGC  AGCACCGTTG  GCTACGGGAG  TACTGGCCGA  TATGGCCGCT  GAAGCTGAGC  CACTATCTGA  CGTTATGCAC
```

FIG. 3-Page 4

pCMV-NS35

1441 TATTTACAAA TTCACATATA CAACAACGCC GTCCCCCGTG CCCGCCAGTT TTATTAAACA TAGCCTGGGA TCTCCGACAT
       ATAAATGTTT AAGTGTATAT GTTGTTGCGG CAGGGGGCAC GGGCGGTCAAA AATAATTTGT ATCGGCACCCT AGAGGCTGTA

1521 CTCGGGTACG TGTTCCGGAC ATGGGCTCTT CTCCGGTAGC GGCGGGAGCTT CCACATCCGA GCCCTGGTCC CATCCGTCCA
       GAGCCCATGC ACAAGGCCTG TACCCGAGAA GAGGCCATCG CCGCCCTCGAA GGTGTAGGCT CGGGACCAGG GTAGGCAGGT

1601 GCGGCTCATG GTCGCCTCGGC AGCTCCTTGC TCCTAACAGT GGAGGCCAGA CTTAGGCACA GCACAATGCC CACCACCACC
       CGCCGAGTAC CAGCGGAGCCG TCGAGGAACG AGGATTGTCA CCTCCGGTCT GAATCCGTGT CGTGTTACGG GTGGTGGTGG

1681 AGTGTGCCGC ACAAGGCCGT GGCGGTAGGG TATGTGTCTG AAAATGAGCT CGGAGATTGG GCTCGCCACCT GGACGCCAGAT
       TCACACGGCG TGTTCCGGCA CCGCCATCCC ATACACAGAC TTTTACTCGA GCCTCTAACC CGAGCGGTGGA CCTGCGTCTA

1761 GGAAGACTTA AGGCAGCGGC AGAAGAAGAT GCAGGCAGCT GAGTTGTTGT ATTCTGATAA GAGTCAGAGG TAACTCCCGT
       CCTTCTGAAT TCCGTCGCCG TCTTCTTCTA CGTCCGTCGA CTCAACAACA TAAGACTATT CTCAGTCTCC ATTGAGGGCA

1841 TGCGGGTGCTG TTAACGGTGG AGGGCAGTGT AGTCTGAGCA GTACTCCGTTG CTGCCCGCCCG CGCCACCAGA CATAATAGCT
       ACGCCCACGAC AATTGCCACC TCCCGTCACA TCAGACTCGT CATGAGGCAAC GACGGGCGGC GCGGTGGTCT GTATTATCGA

  +2
                                        M A   A

                                         EcoRI

1921 GACAGACTAA CAGACTGTTC CTTTCCATGG GTCTTTTCTG CAGTCACCGT CGTCGACCTA AGAATTCACC ATGGCTGCAT
       CTGTCTGATT GTCTGACAAG GAAAGGTACC CAGAAAAGAC GTCAGTGGCA GCAGCTGGAT TCTTAAGTGG TACCGACGTA

  +2 Y A A   Q   G Y K   V L V L N P S   V A A   T L G F G A Y   M S K
2001 ATGCAGCTCA GGGCTATAAG GTGCTAGTAC TCAACCCCTC TGTTGCTGCA ACACTGGGCT TTGGTGCTTA CATGTCCAAG
       TACGTCGAGT CCCGATATTC CACGATCATG AGTTGGGGAG ACAACGACGT TGTGACCCGA AACCACGAAT GTACAGGTTC

FIG. 3-Page 3

pCMV–NS35

```
    +2  G  A  K  D     V  R  C     H  A  R  K     A  V  T  H  I  N     S  V  W  K     D  L  L     E  D  N
  5841  GGGCAAAAGA  CGTCCGTTGC  CATGCCAGAA  AGGCCGTAAC  CCACATCAAC  TCCGTGTGGA  AAGACCTTCT  GGAAGACAAT
        CCCGTTTTCT  GCAGGCAACG  GTACGGTCTT  TCCGGCATTG  GGTGTAGTTG  AGGCACACCT  TTCTGGAAGA  CCTTCTGTTA

    +2  V  T  P  I  D  T  T     I  M  A     K  N  E  V     F  C  V     Q  P  E     K  G  G  R     K  P  A
  5921  GTAACACCAA  TAGACACTAC  CATCATGGCT  AAGAACGAGG  TTTTCTGCGT  TCAGCCTGAG  AAGGGGGGTC  GTAAGCCAGC
        CATTGTGGTT  ATCTGTGATG  GTAGTACCGA  TTCTTGCTCC  AAAAGACGCA  AGTCGGACTC  TTCCCCCCAG  CATTCGGTCG

    +2  R  L  I     V  F  P  D     L  G  V     R  V  C     E  K  M  A     L  Y  D     V  V  T     K  L  P
  6001  TCGTCTCATC  GTGTTCCCCG  ATCTGGGCGT  GCGCGTGTGC  GAAAAGATGG  CTTTGTACGA  CGTGGTTACA  AAGCTCCCCT
        AGCAGAGTAG  CACAAGGGGC  TAGACCCGCA  CGCGCACACG  CTTTTCTACC  GAAACATGCT  GCACCAATGT  TTCGAGGGGA

    +2  L  A  V  M     G  S  S     Y  G  F  Q     Y  S  P     G  Q  R     V  E  F  L     V  Q  A     W  K  S
  6081  TGGCCGTGAT  GGGAAGCTCC  TACGGATTCC  AATACTCACC  AGGACAGCGG  GTTGAATTCC  TCGTGCAAGC  GTGGAAGTCC
        ACCGGCACTA  CCCTTCGAGG  ATGCCTAAGG  TTATGAGTGG  TCCTGTCGCC  CAACTTAAGG  AGCACGTTCG  CACCTTCAGG
                                                                          EcoRI
                                                                          -----

    +2  K  K  T  P     M  G  F     S  Y  D     T  R  C  F     D  S  T     V  T  E     S  D  I  R     T  E  E
  6161  AAGAAAACCC  CAATGGGGTT  CTCGTATGAT  ACCCGCTGCT  TTGACTCCAC  AGTCACTGAG  AGCGACATCC  GTACGGAGGA
        TTCTTTTGGG  GTTACCCCAA  GAGCATACTA  TGGGCGACGA  AACTGAGGTG  TCAGTGACTC  TCGCTGTAGG  CATGCCTCCT

    +2  A  I  Y     Q  C  C  D     L  D  P     Q  A  R     V  A  I  K     S  L  T     E  R  L     Y  V  G
  6241  GGCAATCTAC  CAATGTTGTG  ACCTCGACCC  CCAAGCCCGC  GTGGCCATCA  AGTCCCTCAC  CGAGAGGCTT  TATGTTGGGG
        CCGTTAGATG  GTTACAACAC  TGGAGCTGGG  GGTTCGGGCG  CACCGGTAGT  TCAGGGAGTG  GCTCTCCGAA  ATACAACCCC

    +2  G  P  L  T     N  S  R     G  E  N  C     G  Y  R     R  C  R     A  S  G  V     L  T  T     S  C  G
  6321  GCCCTCTTAC  CAATTCAAGG  GGGGAGAACT  GGGGCTATCG  CAGGTGCCGC  GCGAGCGGCG  GCCTCGCCCG  TACTGACAAC  TAGCTGTGGT
        CGGGAGAATG  GTTAAGTTCC  CCCCTCTTGA  CCCCGATAGC  GTCCACGGCG  CGCTCGCCGC  CGGAGCGGGC  ATGACTGTTG  ATCGACACCA
```

FIG. 3–Page 11

pCMV-NS35

721 GCCTGGCATT ATGCCCAGTA CATGACCTTA CGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC
    CGGACCGTAA TACGGGTCAT GTACTGGAAT GCCCTGAAAG GATGAACCGT CATGTAGATG CATAATCAGT AGCGATAATG

801 CATGGTGATG CGGTTTTGGC AGTACACCAA TGGGCGTGGA TAGGGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA
    GTACCACTAC GCCAAAACCG TCATGTGGTT ACCCGCACCT ATCGGCCAAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT

881 TTGACCTCAA TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ATAACCCCGC CCCGTTGACG
    AACTGCAGTT ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TATTGGGGCG GGGCAACTGC

961 CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG
    GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGC AAATCACTTG GCAGTCTAGC GGACCTCTGC

1041 CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC TCCCGGCCCG GGAACGGTGC ATTGGAACGC
     GGTAGGTGCG ACAAAACTGG AGGTATCTTC TGTGGCCCTG GCTAGGTCGG AGGGCCGGGC CCTTGCCACG TAACCTTGCG

1121 GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCCTATAG ACTCTATAGG CACACCCCTT TGGCTCTTAT GCATGCTATA
     CCTAAGGGGC ACGGTTCTCA CTGCATTCAT GGCGGATATC TGAGATATCC GTGTGGGGAA ACCGAGAATA CGTACGATAT

1201 CTGTTTTTGG CTTGGGGCCT ATACACCCCC GCTCCTTATG CTATAGGTGA TGGTATAGCT TAGCCTATAG GTGTGGGTTA
     GACAAAAACC GAACCCCGGA TATGTGGGGG CGAGGAATAC GATATCCACT ACCATATCGA ATCGGATATC CACACCCAAT

1281 TTGACCATTA TTGACCACTC CCCTATTGGT GACGATACTT TCCATTACTA ATCCATAACA TGGCTCTTTG CCACAACTAT
     AACTGGTAAT AACTGGTGAG GGGATAACCA CTGCTATGAA AGGTAATGAT TAGGTATTGT ACCGAGAAAC GGTGTTGATA

1361 CTCTATTGGC TATATGCCAA TACTCTGTCC TTCAGAGACT GACACGGACT CTGTATTTTT ACAGGATGGG GTCCATTTAT
     GAGATAACCG ATATACGGTT ATGAGACAGG AAGTCTCTGA CTGTGCCTGA GACATAAAAA TGTCCTACCC CAGGTAAATA

FIG. 3-Page 2

pCMV-NS35

```
  1   TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT
      AGCGCGCAAA GCCACTACTG CCACTTTTGG AGACTGTGTA CGTCGAGGGC CTCTGCCAGT GTCGAACAGA CATTCGCCTA

 81   GCCGGGAGCA GACAAGCCCG TCAGGGGGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA
      CGGCCCTCGT CTGTTCGGGC AGTCCCCGC AGTCGCCCAC AACCGCCCAC AGCCCCGACC GAATTGATAC GCCGTAGTCT
                                                                              StuI
                                                                              -------

161   GCAGATTGTA CTGAGAGTGC ACCATATGAA GCTTTTTGCA AAAGCCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG
      CGTCTAACAT GACTCTCACG TGGTATACTT CGAAAAACGT TTTCGGATCC GGAGGTTTTT TCGGAGGAGT GATGAAGACC

241   AATAGCTCAG AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAAT TAGTCAGCCA TGGGGGCGAG AATGGGCGGA
      TTATCGAGTC TCCGGCTCCG CCGGAGCCGG AGACGTATTT ATTTTTTTTA ATCAGTCGGT ACCCCGCCTC TTACCCGCCT

321   ACTGGGCGGG GAGGGAATTA TTGGCTATTG GCCATTGCAT ACGTTGTATC TATATCATAA TATGTACATT TATATTGGCT
      TGACCCGCCC CTCCCTTAAT AACCGATAAC CGGTAACGTA TGCAACATAG ATATAGTATT ATACATGTAA ATATAACCGA

401   CATGTCCAAT ATGACCGCCA TGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT
      GTACAGGTTA TACTGGCGGT ACAACTGTAA CTAATAACTG ATCAATAATT ATCATTAGTT AATGCCCCAG TAATCAAGTA

481   AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG CCCAACGACC CCCGCCCATT
      TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGCGGGTAA

561   GACGTCAATA ATGACGTATG TTCCCATAGT AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT
      CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTC ATAAATGCCA

641   AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTCCGCCC CCTATTGACG TCAATGACGG TAAATGGCCC
      TTTGACGGGT GAACCGTCAT GTAGTTCACA TAGTATACGG TTCAGGCGGG GGATAACTGC AGTTACTGCC ATTTACCGGG
```
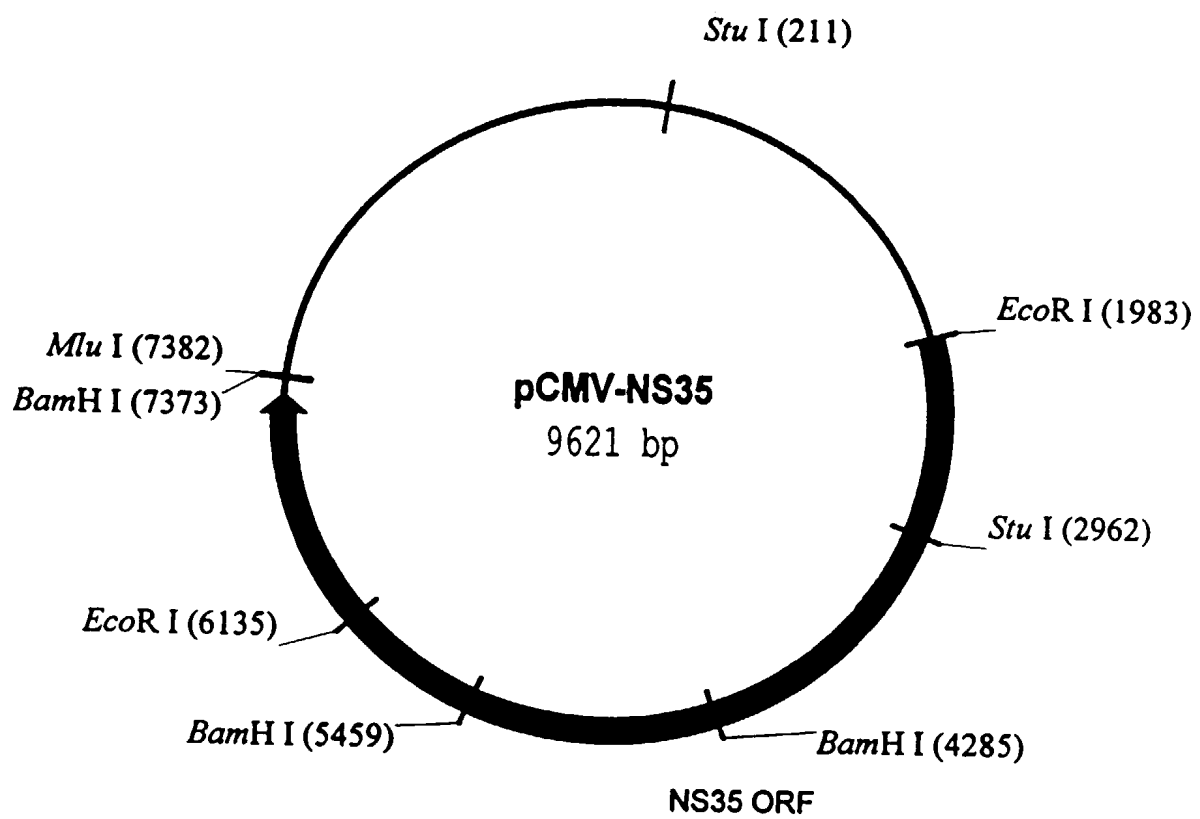
FIG. 3-Page 1

Stu I (211)

EcoR I (1983)

Mlu I (7382)
BamH I (7373)

pCMV-NS35
9621 bp

Stu I (2962)

EcoR I (6135)

BamH I (5459)

BamH I (4285)

NS35 ORF

FIG. 2

Cloning Scheme for Generating pCMV-NS35

NS34A

```
        EcoRI        StuI  BamHI
```

+

delNS35

```
        EcoRI  StuI           MluI
```

NS35

```
        EcoRI        StuI        MluI
```
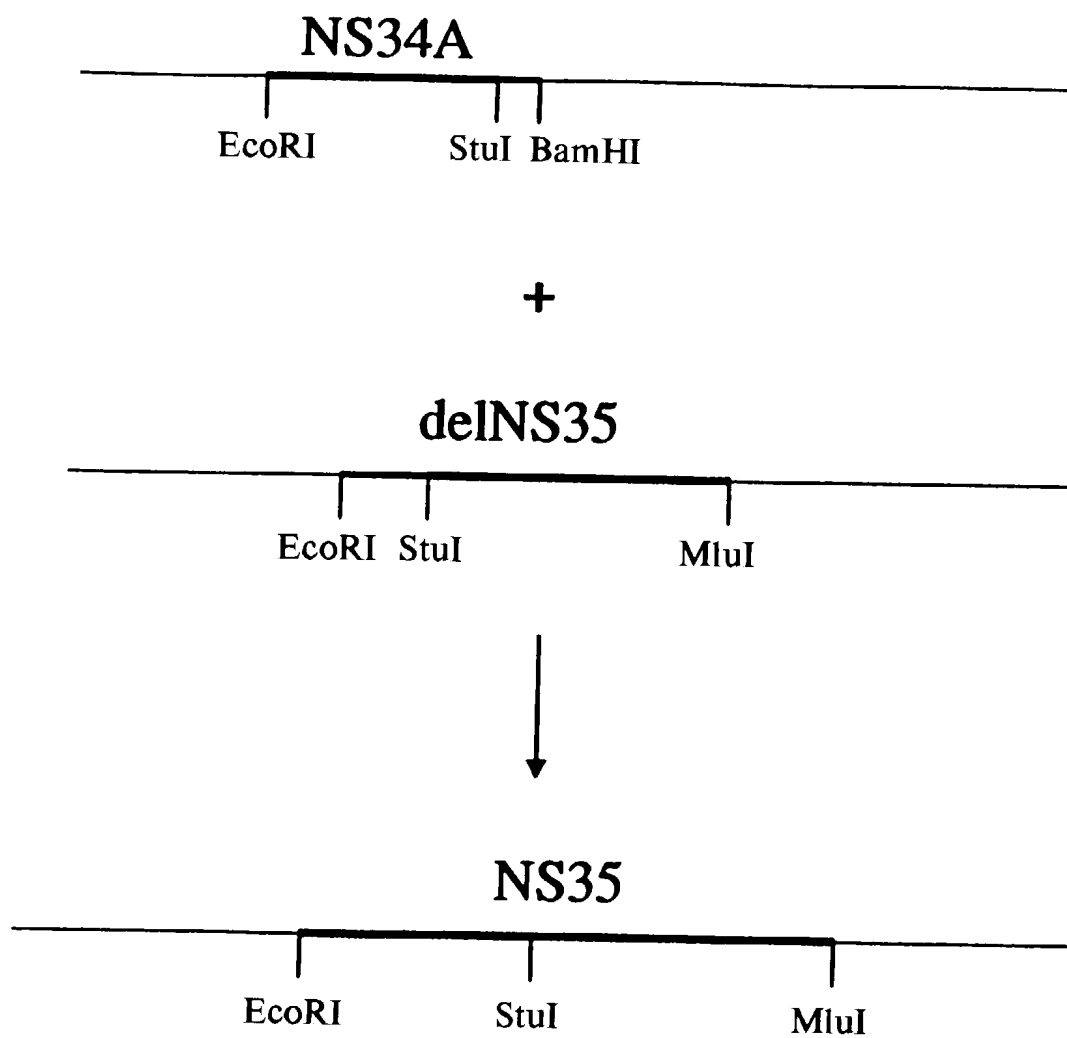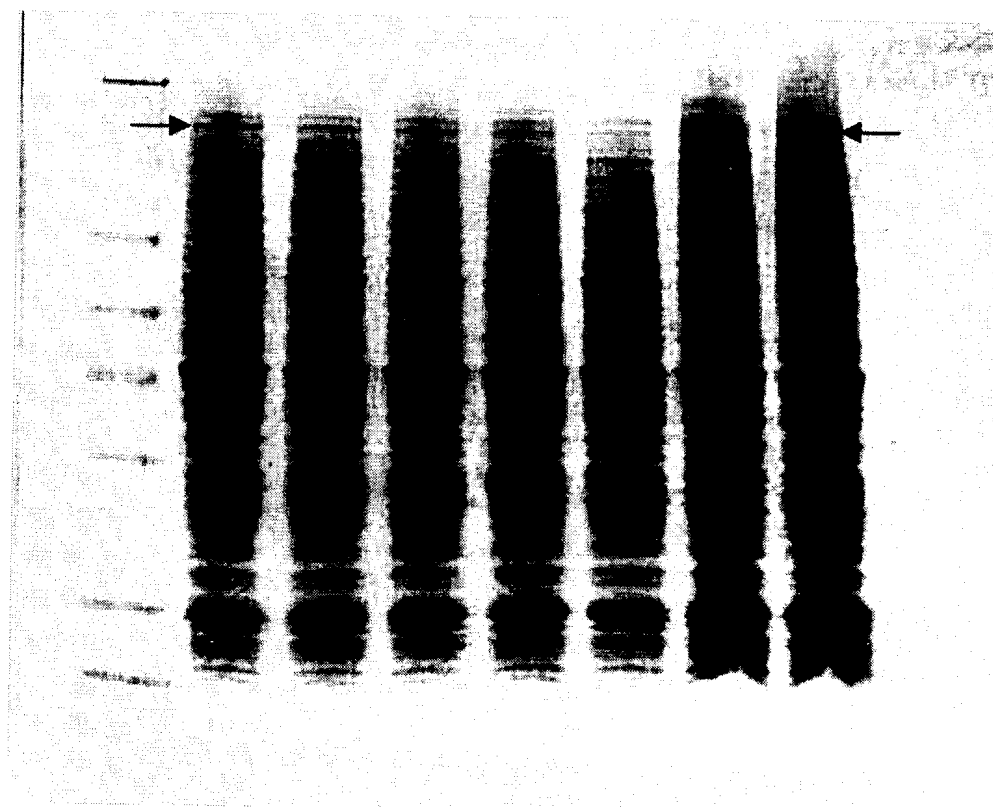
FIG. 1

FIG. 23

5449 APAI,

```
       GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
5462   GGTGTGCGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
       CCACACGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
       ^                 ^                         ^        ^
5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,

       IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
5522   ATCCCCAAGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCC
       TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
                                 ^          ^     ^   ^
5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,

       LeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
5582   CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGG
       GAGATACCGTTACTCCCGACGCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

       ProSerTrpGlyProThrAspProArgArgArgSerArgAsnLeuGlyLysValIleAsp
5642   CCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGAT
       GGATCGACCCCGGGGTGTCTGGGGGCCGCATCCAGCGCGTTAAACCCATTCCAGTAGCTA
       ^                                                         ^
5650 APAI, 5696 CLAI,

       ThrLeuThrCysGlyPheAlaAspLeuMetGlyTyrIleProLeuValGlyAlaProLeu
5702   ACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTT
       TGGGAATGCACGCCGAAGCGGCTGGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA
                         ^                             ^      ^
5724 HGIE2, 5750 KAS1 NARI, 5756 ECON1,

       GlyGlyAlaAlaArgAlaOC AM
5762   GGAGGCGCTGCCAGGGCCTAATAGTCGAC
       CCTCCGCGACGGTCCCGGATTATCAGCTG
                           ^
5785 SALI,
```

FIG. 22-Page 10

A DOCPHOENIX

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APPL PARTS

_____ IMIS _____
Internal Misc Paper

_____ LET _____
Misc Incoming Letter

_____ 371P _____
PCT Papers in a 371Application

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Amendment Including Elections

_____ ABST _____
Abstract

_____ ADS _____
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Appendix

_____ ARTIFACT _____
Artifact

_____ BIB _____
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_____ CLM _____
Claim

_____ COMPUTER _____
Computer Program Listing

_____ CRFL _____
All CRF Papers for Backfile

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Terminal Disclaimer Filed

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Drawings

_____ FOR _____
Foreign Reference

_____ FRPR _____
Foreign Priority Papers

_____ IDS _____
IDS Including 1449

_____ NPL _____
Non-Patent Literature

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Oath or Declaration

_____ PET. _____
Petition

_____ RETMAIL _____
Mail Returned by USPS

_____ SEQLIST _____
Sequence Listing

_____ SPEC _____
Specification

_____ SPEC NO _____
Specification Not in English

_____ TRNA _____
Transmittal New Application

OUTGOING

_____ CTMS _____
Misc Office Action

_____ 1449 _____
Signed 1449

_____ 892 _____
892

_____ ABN _____
Abandonment

_____ APDEC _____
Board of Appeals Decision

_____ APEA _____
Examiner Answer

_____ CTAV _____
Count Advisory Action

_____ CTEQ _____
Count Ex parte Quayle

_____ CTFR _____
Count Final Rejection

_____ CTNF _____
Count Non-Final

_____ CTRS _____
Count Restriction

_____ EXIN _____
Examiner Interview

_____ M903 _____
DO/EO Acceptance

_____ M905 _____
DO/EO Missing Requirement

_____ NFDR _____
Formal Drawing Required

_____ NOA _____
Notice of Allowance

_____ PETDEC _____
Petition Decision

INCOMING

_____ AP.B _____
Appeal Brief

_____ C.AD _____
Change of Address

_____ N/AP _____
Notice of Appeal

_____ PA.. _____
Change in Power of Attorney

_____ REM _____
Applicant Remarks in Amendment

_____ XT/ _____
Extension of Time filed separate

Internal

_____ SRNT _____
Examiner Search Notes

_____ CLMPTO _____
PTO Prepared Complete Claim Set

_____ ECBOX _____
Evidence Copy Box Identification

_____ WCLM _____
Claim Worksheet

_____ WFEE _____
Fee Worksheet

File Wrapper

_____ FWCLM _____
File Wrapper Claim

_____ IIFW _____
File Wrapper Issue Information

_____ SRFW _____
File Wrapper Search Info

REV 7/02/03

FIGURE 1

Cloning Scheme for Generating pCMV-NS35